


```

#cross-references MUID:90111618
#accession PL0273
##molecule_type mRNA
#residues 1-112 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
  1-23      #region framework 1\\
  24-39     #region Complementarity-determining 1\\
  40-54     #region framework 2\\
  55-61     #region Complementarity-determining 2\\
  62-93     #region framework 3\\
  94-102    #region Complementarity-determining 3\\
  103-112   #region framework 4\\
  SUMMARY    #length 112 #checksum 8934

Query Match      81.4%: Score 659; DB 2; Length 112;
Best Local Similarity 81.3%; Pred. No. 1.00e 84;
Matches 91; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db  1 DVMQTQPLTSLVIGQPASISCRSSQSILLYRNGKTYLNWLQRPQSPKRLLYLVSKLD 60
Qy  1 DVMQTQSPSLLVLGQPASISCRSSQSILLYRNGKTYLNWLQRPQSPQPLIYLVSKE 60

Db  61 SGYPDRFTSGSGTDFTLKISRYEAEDLGYYCVQGTHPWTFGGTGLEIK 112
Qy  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 112

Db  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 112
Qy  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 112

RESULT 3          S22902 #type complete
ENTRY          Ig kappa chain V region - human
TITLE          #formal_name Homo sapiens #common_name man
ORGANISM        DATE 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
               16-Aug-1996
ACCESSIONS S22902
REFERENCE
#authors Chastagner, P.; Theze, J.; Zouali, M.
#journal Gene (1991) 101:305-306
#title Cloning of a gene encoding a lupus-associated human
autocatantibody V(K) region using the polymerase chain
reaction and degenerate primers.
#cross-references MUID:91276289
#accession S22902
#status preliminary; translation not shown
##molecule_type mRNA
##residues 1-142 #label CHA
#cross-references EMBL:X56510
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 142 #molecular_weight 15579 #checksum 227

Query Match      80.6%: Score 653; DB 2; Length 142;
Best Local Similarity 84.7%; Pred. No. 9.42e 84;
Matches 94; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db  32 DVMQTQPLSPLPTLGQPASISCRSSQSILYHSDGNTYLNWFQRPQSPRLLYKVSNRD 91
Qy  1 DVMQTQSPSLLVLGQPASISCRSSQSILYHSSGNTYLNWLQRPQSPQPLIYLVSKE 60

Db  92 SGYPDRFTSGSGTDFTLKISRYEAEDGVYICMQGTHWPTFGGTLEI 142
Qy  92 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQGTHWPTFGGTLEI 142

Db  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 111
Qy  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 111

RESULT 4          F30560 #type fragment (28.4.10A) - mouse (fragment)
ENTRY          Ig kappa chain V region #common_name house mouse
TITLE          #formal_name Mus musculus #common_name house mouse
ORGANISM        DATE 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change
               20-Mar-1998
ACCESSIONS F30560
REFERENCE

#authors Matsuda, T.; Kabat, E.A.
#journal J. Immunol. (1989) 142:863-870
#Title Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1-6)extran.
#cross-references MUID:89110062
#accession F30560
#status preliminary
##molecule_type mRNA
##residues 1-113 ##label MAT
#cross-references GB:M24273; NID:9197081; PID:9197082
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 113 #checksum 1877

Query Match      80.0%: Score 648; DB 2; Length 113;
Best Local Similarity 82.1%; Pred. No. 6.09e 83;
Matches 92; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Db  1 DVMTQIPPLTSVIGQPASISCRSSQSILYHSDGNTYLNWLQRPQSPRLLYKVSNRD 60
Qy  1 DVMTQIPPLTSVIGQPASISCRSSQSILYHSSGNTYLNWLQRPQSPQPLIYLVSKE 60

Db  61 SGYPDRFTSGSGTDFTLKISRYEAEDGVYICMQGTHWPTFGGTLEIK 112
Qy  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 112

RESULT 5          S23230 #type fragment
ENTRY          Ig kappa chain precursor V-J region - human (fragment)
TITLE          #formal_name Homo sapiens #common_name man
ORGANISM        DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
               08-Sep-1997
ACCESSIONS S23230
REFERENCE
#authors Kennedy, M.A.
#journal J. Exp. Med. (1991) 173:1033-1036
#title Novel chromosome translocation caused by fusion of
immunoglobulin heavy and light chain genes in a human B
lymphoblastoid cell line.
#cross-references S23230
#status preliminary
##molecule_type DNA
##residues 1-133 ##label KEN
#cross-references EMBL:X55400; NID:933999; PID:934000
GENETICS
#intcons 17/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 133 #checksum 2932

Query Match      79.9%: Score 647; DB 2; Length 133;
Best Local Similarity 84.8%; Pred. No. 8.84e 83;
Matches 95; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Db  21 DVMQTQSPSLLVLGQPASISCRSSQSILYHSDGNTYLNWFQRPQSPRLLYKVSNRD 80
Qy  1 DVMQTQSPSLLVLGQPASISCRSSQSILYHSSGNTYLNWLQRPQSPQPLIYLVSKE 60

Db  81 SGYPDRFTSGSGTDFTLKISRYEAEDGVYICMQGTHWPTFGGTLEIK 132
Qy  61 SGYPDRFTSGSGTDFTLKISGYEAEDGVYICMQFTHPYTFQGTGLEIK 112

RESULT 6          A55491 #type complete
ENTRY          Ig kappa chain V region - mouse (fragment)
TITLE          #formal_name Mus musculus #common_name house mouse
ORGANISM        DATE 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change
               03-May-1996
ACCESSIONS A55491

```

REFERENCE #authors Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; ...
#journal Tramontano, A.; Massey, R.J.; Paul, S.
#title Molecular cloning of a proteolytic antibody light chain.
#accession A55491
#status preliminary
#molecule_type mRNA
##residues 1-112 ##label GAO
#cross-references GB:L34775
#note authors translated the codon TAT for residue 37 as Thr
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 112 #molecular_weight 12252 #checksum 7719

Query Match 79.8%; Score 646; DB 2; Length 112;
Best Local Similarity 81.3%; Pred. No. 1.28e-82;
Matches 91; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Db 1 DVVMTQPLTSLVTGPASESCKSSQSSLIDTDGKTYLIWLLQRGQSPKRILYLVSKLD 60
Qy 1 DVVMTQSPPSLVLTVGPASISCRSSQSSLHSGNTYLNWLLQRGQSPQPLIYLVSKLE 60

Db 61 SGVPDRFTGSSTGDTFLKISVEAEDGVYCWQGTHFPTFGGGTKEIK 112
Qy 61 SGVPDRFTGSSTGDTFLKISVEAEDGVYCMQFTHYPPFGQGTKEIK 112

RESULT 7 C32513 #type complete
#label Ig kappa chain precursor V region (BXW14) - mouse
#formal_name Mus musculus #common_name house mouse
#date 21-May-1990 #sequence_revision 31-Dec-1990 #text_change
20-Mar-1998

ACCESSIONS A94489
REFERENCE Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;
Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,
A.N.
#journal J. Clin. Invest.
#title (1988) 82:852-860
#cross-references MUID:88331394
#molecule_type DNA
#accession C32513
#cross-references GB:M20830; NTID:gi196939; PID:gi196940
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS #length 132 #molecular_weight 14594 #checksum 9719

Query Match 79.8%; Score 646; DB 2; Length 132;
Best Local Similarity 82.1%; Pred. No. 1.28e-82;
Matches 92; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 21 DVVMTQPLTSLVTGPASISCKSSQSSLIDDGKTYLIWLLQRGQSPKRILYLVSKLD 80
Qy 1 DVVMTQSPPSLVLTVGPASISCRSSQSSLHSGNTYLNWLLQRGQSPQPLIYLVSKLE 60

Db 81 SGVPDRFTGSSTGDTFLKISVEAEDGVYCWQGTHFPTFGGGTKEIK 132
Qy 61 SGVPDRFTGSSTGDTFLKISVEAEDGVYCMQFTHYPPFGQGTKEIK 112

RESULT 8 C36259 #type complete
#label Ig kappa chain V region (TE34) - mouse
#formal_name Mus musculus #common_name house mouse
#date 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change
16-Aug-1996

ACCESSIONS A36259
REFERENCE Zilberman, B.; Scherf, T.; Levitt, M.; Anglister, J.

RESULT 9 S22658 #type fragment
#label Ig kappa chain precursor V region (0-81Y) - human (fragment)
#organism Homo sapiens #common_name man
#date 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change
06-Feb-1998

ACCESSIONS S22658
REFERENCE S22657
#authors Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
#journal Nucleic Acids Res. (1992) 20:2601
#title Variable regions of a human anti-DNA antibody O-81 possessing
lupus nephritis-associated idiootype.
#accession S22658
#molecule_type RNA
#residues 1-140 ##label HIR
#cross-references EMBL:A59135
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS #length 140 #text_change
#feature #domain signal sequence #status predicted #label SIG
#product Ig kappa chain (fragment) #status predicted
#label MAT
#accession S22656
#organism Homo sapiens #common_name man
#date 20-Mar-1998 #text_change
#molecule_type DNA
#accession C32513
#cross-references GB:M20830; NTID:gi196939; PID:gi196940
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS #length 132 #molecular_weight 14594 #checksum 9719

Query Match 78.5%; Score 636; DB 2; Length 140;
Best Local Similarity 83.2%; Pred. No. 5.35e-81;
Matches 94; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

Db 21 DVVMTQPLTSLVTGPASISCKSSQSSLIDDGKTYLIWLLQRGQSPKRILYLVSKLD 80
Qy 1 DVVMTQSPPSLVLTVGPASISCRSSQSSLHSGNTYLNWLLQRGQSPQPLIYLVSKLE 60

Db 81 SGVPDRFTGSSTGDTFLKISVEAEDGVYCMQHTHWSPITFGCTRLEIK 133
Qy 61 SGVPDRFTGSSTGDTFLKISVEAEDGVYCMQFTHYPPFGQGTKEIK 112

RESULT 10 S49572 #type fragment
#label Ig kappa chain precursor - human (fragment)
#organism Homo sapiens #common_name man
#date 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change
20-Mar-1998

ACCESSIONS S49572
REFERENCE Giachino, C.; Padovan, E.; Lanaveccchia, A.
#authors Submitted to the EMBL Data Library November 1994

#description k+1+ dual receptor B cells are present in the human peripheral repertoire.

#accession S4572

#status preliminary

#molecule_type mRNA

#residues 1-114 #label GIA

#cross-references EMBL:146626; NID:9575261; PID:9575262

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

SUMMARY #length 114 #checksum 9334

Query Match Score 635; DB 2; Length 114;

Best Local Similarity 82.3%; Pred. No. 7.76e-11;

Matches 9; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

CLASSIFICATION KEYWORDS

FEATURES

FEATURE 1-20

21-133 #domain signal sequence #status predicted #label SIG\

predicted Ig kappa chain V-II region (RPMI) #status

#region framework 1\

#domain immunoglobulin homology #label IMM\

#superfamily immunoglobulin V region; immunoglobulin homology

heterotetramer; immunoglobulin

Db 1 DVVMTQSPLSIPLVQPASTISCRSSQSLVYTQDGNTYLNWFQQRPGSPRILKXVSNRD 60

Qy 1 DVVMTQSPPSLVLVQPASTISCRSSQSLVHSSGNTYLNLWLRQGQSPOPLIVLVSKE 60

Db 61 SGVPDRFGSGSGTDFTLKISRVEAEDGVIXCIGOTHNWQTYTFGGTKEIK 113

Qy 61 SGVPDRFGSGSGTDFTLKISRVEAEDGVYTCMOTHTYTFGGTKEIK 112

RESULT 11

ENTRY S40312 #type complete

ORGANISM #formal_name Homo sapiens #common_name man

DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 08-Sep-1997

ACCESSIONS S40312

REFS

#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. (1993) 23:248-2271

#title Expressed human immunoglobulin chi genes and their hypermutation.

#accession S40312

#status preliminary; translation not shown

#molecule_type mRNA

#residues 1-126 #label KLE

#cross-references EMBL:X72427; NID:9441312; PID:9441313

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS

SUMMARY #length 126 #molecular_weight 13744 #checksum 4861

Query Match Score 78.3%; DB 2; Length 126;

Best Local Similarity 80.4%; Pred. No. 1.13e-80;

Matches 90; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

CLASSIFICATION KEYWORDS

FEATURES

FEATURE 1-126 #domain signal sequence #status predicted #label SIG\

predicted Ig kappa chain V region; immunoglobulin homology

heterotetramer; immunoglobulin

Db 14 DVVMTQSPPSLVLVQPASTISCRSSQSLVHSSGNTYLNLWLRQGQSPOPLIVLVSKE 73

Qy 1 DVVMTQSPPSLVLVQPASTISCRSSQSLVHSSGNTYLNLWLRQGQSPOPLIVLVSKE 60

Db 74 SGVPDRFGSGAGTDFTLKISRVEAEDGVYTCMOTHTYTFGGTKEIK 125

Qy 61 SGVPDRFGSGSGTDFTLKISRVEAEDGVYTCMOTHTYTFGGTKEIK 112

RESULT 12

ENTRY K2HURP #type complete

TITLE Ig kappa chain precursor V-II region (RPMI) - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997

ACCESSIONS A01890

REFERENCE A93388

#authors Klöbeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.

#journal Nucleic Acids Res. (1985) 13:6499-6513

#title Human immunoglobulin kappa light chain genes of subgroups II and III

#cross-references MUID:86041852

#accession A01890

#molecule_type DNA

Query Match Score 78.0%; DB 2; Length 112;

Best Local Similarity 75.9%; Pred. No. 2.37e-80;

Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

A vertical column of five dashed-line outlines of the letter 'E'. The outlines are arranged vertically, with each outline slightly offset to the right of the previous one. The first four outlines are standard 'E' shapes, while the fifth outline is a stylized, more abstract version of the letter.

Release 3.1A John F. Collins, Biocomputing Research Unit.
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protein - protein database search, using Smith-Waterman algorithm

srch_pp	on:	Thu Jan 14 17:10:34 1999:	MaPar time 6.92 Seconds	434.138 Million cell updates/sec
			molecular output not generated.	

>US-08-477-988B-88
(1-112) from US08477989B.pep

SCHNEIDER, H. & FRIEDRICHSON, J. A. / THE CROWN TABLE 112

Gap 11

arched: 74019 seqs, 26840295 residues

st-processing: Minimum Match 08

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database: swiss-prot35

Freq. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1.32e-1

2.80e-1

1.60e-1

8.388-1

5.60e-1

1.10e-9

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1.68e-9:

5.01e-9

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1.33e-8

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE; 84191506.
 RA KLOBECK H.G.; SOLOMON A.; ZACHAU H.G.;
 RL NATURE 309:73-76(1984).
 EMBL; 200009; ; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HGM.
 DR HSSP; P01679; ICPV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON_TER 1
 SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION (GM607).
 FT DOMAIN 5 27 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 28 43 FRAMEWORK 1.
 FT DOMAIN 44 58 FRAMEWORK 2.
 FT DOMAIN 59 65 FRAMEWORK 3.
 FT DOMAIN 66 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 106 FRAMEWORK 4.
 FT DOMAIN 107 116 BY SIMILARITY.
 FT DISULFID 27 97
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; E09E9ACC CRC32;

Query Match 73.5%; Score 595; DB 1; Length 117;
 Best Local Similarity 78.6%; Pred. No. 2.80e-112; Indels 0; Gaps 0;
 Matches 88; Conservative 8; Mismatches 16; Delins 0; Gaps 0;

Db 5 DIVMTQSPSLPVTPGEAPASCRSSQSLHSGNCGYNTDYLWQLQPOQSPQLIYLGNSRA 64
 Qy 1 DIVMTQSPSLPVTPGEAPASCRSSQSLHSGNCGYNTDYLWQLQPOQSPQLIYLGNSRA 60

Db 65 SGVPDRFGSGSGTDFTLKISRVEAEDGVYICMAGLQPQTFGQQTKVEIK 116
 Qy 61 SGVPDRFGSGSGTDFTLKISRVEAEDGVYICMAGLQPQTFGQQTKVEIK 112

RESULT 6
 ID KV2A_HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (CUM).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.

RX MEDLINE; 68242259.
 RA HILSCHMANN N.;
 RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 96 AND 97.
 RX MEDLINE; 70063440.
 RA HILSCHMANN N.;
 RL NATURWISSENSCHAFTEN 56:195-205(1969).
 CC - THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC - THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01885; K2HGM.
 DR HSSP; P01607; IGG1.

KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DISULFID 24 95 BY SIMILARITY.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 5500220A CRC32;

Query Match 72.8%; Score 590; DB 1; Length 115;
 Best Local Similarity 77.9%; Pred. No. 4.44e-111; Indels 1; Gaps 1;

Db 2 DIVMTQSPSLPVTPGEAPASCRSSQSLHSGNCGYNTDYLWQLQAGSPQLIYLSYR 61

QY ...1.DIVMTQSPSLPVTPGEAPASCRSSQSLHSS-GNTYLNWLQRPGQSPQPLIYLVSKL 59
 Db 62 ASGPDRFGSGSGTDFTLKISRVEAEDGVYICMAGLQPQTFGQQTKVEIK 114
 QY 60 ESGVPDRFGSGSGTDFTLKISRVEAEDGVYICMAGLQPQTFGQQTKVEIK 112
 RESULT 7
 ID KV2C_HUMAN STANDARD; PRT; 112 AA.
 AC P01616;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (MIL).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RA DREYER W.J.; GRAY W.R.; HOOD L.E.;
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 32:353-367(1967).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC - THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01887; K2HGM.
 DR HSSP; P01679; 1CBV.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 2 38 FRAMEWORK 2.
 FT DOMAIN 3 53 FRAMEWORK 3.
 FT DOMAIN 4 60 FRAMEWORK 4.
 FT DOMAIN 5 92 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 102 111 FRAMEWORK 4.
 FT NON_TER 112 112 BY SIMILARITY.
 SQ SEQUENCE 112 AA; 12055 MW; C487DFDF CRC32;
 Query Match 70.5%; Score 571; DB 1; Length 112;
 Best Local Similarity 67.9%; Pred. No. 1.60e-106;
 Matches 76; Conservative 21; Mismatches 14; Indels 1; Gaps 1;

Db 1 DIVMTQSPSLPVTPGEAPASCRSSQSLHSGNCGYNTDYLWQLQAGSPQLIYLSYR 59
 Qy 1 DIVMTQSPSLPVTPGEAPASCRSSQSLHSGNCGYNTDYLWQLQAGSPQLIYLSYR 60
 Db 60 SGVPNRFGSGSGTDFTLKISRVAZBVGYYCMAGLQPQTFGQQTKVEIK 111
 Qy 61 SGVPDRFGSGSGTDFTLKISRVEAEDGVYICMAGLQPQTFGQQTKVEIK 112
 RESULT 8
 ID KV2G_MOUSE STANDARD; PRT; 113 AA.
 AC P01611;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (26-10).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 83178921.
 RA NOVOTNY J.; MARGOLIES M.N.;
 RL BIOCHEMISTRY 22:1153-1158(1983).
 CC - THIS CHAIN WAS ISOLATED FROM AN IgG2A HYBRIDOMA PROTEIN THAT
 CC BINDS DIGOXIN.
 DR PIR; A01914; KVMS26.
 DR HSSP; P01607; IGG1.
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.

Query Match 9 Score 558; DB 1; Length 113;
 Best Local Similarity 73.2%; Pred. No. 2.06e-103;
 Matches 82; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Result 9 ID KV2_MOUSE STANDARD PRT; 113 AA.

ID P03976; AC P03976; DT 23-OCT-1986 (REL. 02, CREATED);
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (17S29.1).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN SEQUENCE.
 RC TISSUE HYBRIDOMA;
 RX MEDLINE; 83055101.
 RA AEBERSOLD R., HOPPE SEYLER'S Z., GRUTTER T., CHANG J.Y., BRAUN D.G.;
 RL HOPPE SEYLER'S Z., PHYSIOL. CHEM. 365:1375-1383(1984).
 CC -1- ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
 DR PIR; A01912; KWM17.
 DR HSSP; P01679; 1CBV.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.

FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 FRAMEWORK 2.
 FT DOMAIN 40 54 FRAMEWORK 3.
 FT DOMAIN 55 61 FRAMEWORK 4.
 BY SIMILARITY.

Sequence 113 AA; 12273 MW; 58372CBE CRC32;

Query Match 10 Score 558; DB 1; Length 113;
 Best Local Similarity 70.1%; Pred. No. 8.36e-106;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Result 10 ID KV2_MOUSE STANDARD PRT; 112 AA.

ID P01629; AC P01629; DT 21-JUL-1986 (REL. 01, CREATED);
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-IV REGION (LEN).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC PRIMATES.
 RN [1].
 RP SEQUENCE.
 RX MEDLINE; 7604342.
 RA SCHNEIDER M., HILSCHMANN N.;
 RL HOPPE SEYLER'S Z., PHYSIOL. CHEM. 356:507-557(1975).
 RN [2].

Query Match 11 Score 552; DB 1; Length 112;
 Best Local Similarity 72.3%; Pred. No. 5.60e-102;
 Matches 81; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Result 11 ID KV4A_HUMAN STANDARD PRT; 114 AA.

ID P01625; AC P01625; DT 21-JUL-1986 (REL. 01, CREATED);
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-IV REGION (LEN).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC PRIMATES.
 RN [1].
 RP SEQUENCE.
 RX MEDLINE; 7604342.
 RA SALOMON A.;
 RL SUBMITTED (AUG-1996) TO THE SWISS-PROT DATA BANK.
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01903; KAHULN.
 DR HSSP; P01607; 1MCP.
 KW IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.

FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 40 FRAMEWORK 2.
 FT DOMAIN 41 55 FRAMEWORK 3.
 FT DOMAIN 56 62 FRAMEWORK 4.
 FT DOMAIN 63 94 FRAMEWORK 5.
 FT DOMAIN 95 101 FRAMEWORK 6.
 FT DOMAIN 102 113 FRAMEWORK 7.
 BY SIMILARITY.

Sequence 114 AA; 12390 MW; 6A4552AE CRC32;

Query Match 12 Score 558; DB 1; Length 113;
 Best Local Similarity 73.2%; Pred. No. 2.06e-103;
 Matches 82; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Result 12 ID KV2_MOUSE STANDARD PRT; 112 AA.

ID P01629; AC P01629; DT 21-JUL-1986 (REL. 01, CREATED);
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT ~01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

Db 61 SGYSDRSGSGSGTDFLISRYKAEDGVYCOQLVEYPLIFGAGTKEIK 112
 |:||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 61 SGYPDRESGSGSGTDFLKISGEAEDGVYCMQFTHYPTEFGQTKLEIK 112

RESULT 15

ID	KV3J_MOUSE	STANDARD;	PRT;	111 AA.
AC	P01662;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).			
OS	MUS MUSCULUS (MOUSE)			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE (ABPC 22).			
RX	MEDLINE: 79012520.			
RA	MCKEAN D.J., BELL M., POTTER M.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).			
RN	[2]			
RP	SEQUENCE (PC 9245).			
RX	MEDLINE: 79073152.			
RA	WEIGERT M., GATMATTAN L., LOH E., SCHILLING J., HOOD L.E.;			
RL	NATURE 276:795-790(1978);			
CC	-1- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.			
DR	PIR: A01935; KVM3M6.			
DR	HSSP; P01679; IACC.			
KW	IMMUNOGLOBULIN V REGION.			
DOMAIN	1	23		
FT	COMPLEMENTARITY-DETERMINING 1.			
DOMAIN	24	38		
FT	FRAMEWORK 2.			
DOMAIN	39	53		
FT	COMPLEMENTARITY-DETERMINING 2.			
DOMAIN	54	60		
FT	FRAMEWORK 3.			
DOMAIN	61	92		
FT	COMPLEMENTARITY-DETERMINING 3.			
DOMAIN	93	101		
FT	FRAMEWORK 4.			
DISULFID	102	111		
FT	BY SIMILARITY.			
NON TER	23	92		
FT				
SEQUENCE	111 AA;	12041 MR;	711C54A CRC32;	

Query Match 63.0%; Score 510; DB 1; Length 111;
 Best Local Similarity 63.4%; Pred. No. 5.63e-92;
 Matches 71; Conservative 18; Mismatches 22; Indels 1; Gaps 1;

Db 1 NTVLTQSPASLAVSLGQRATISCRASESV-DSVGNSEMFHWYQOKPGQPKLILYLASM 59
 :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 1 DYMNTQSPSLVLGQPASISCRSSQSLHSGNTYLNWLQRPQGSQPKLILYLSKLE 60

Db 60 SGYPARFEGSGSGTDFLTIDPVEADDATYCQNNNDPYFFGGTKEIK 111
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 61 SGYPDRESGSGSGTDFLKISGEAEDGVYCMQFTHYPTEFGQTKLEIK 112

Search completed: Thu Jan 14 17:10:43 1999
 Job time : 9 secs.

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=PBL;
 RA ITOH K., SUZUKI T.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL: AB006843; D1023042;
 DR PFAM: PF00047; Ig.
 FT NON_TER 118 118 MW: CECE07A CRC32;
 SQ SEQUENCE 118 AA: 12804 MW: CECE07A CRC32;

Query Match 3 ELVLTOSPLSPVTPGEPASISCRSSQSLIHSNGNNEMDWTLQRPGQSPQLIYLGNSRA 62
 Matches 89; Best Local Similarity 76.7%; Score 621; DB 4; Length 118;
 Pred. No. 1. 80e-118; FT Non-Ter 119 119 MW: 6B5A6578 CRC32;
 Mismatches 10; Indels 0; Gaps 0; FT Signal 1 19
 FT Chain 20 >119
 FT Non-Ter 119 119
 SQ Sequence 119 AA: 13079 MW: 6B5A6578 CRC32;
 FT Potential.
 IG Kappa Chain.

Query Match 3 ELVLTOSPLSPVTPGEPASISCRSSQSLIHSNGNTLYLHWYLQKGQSPKLIIYKYSNRF 79
 Matches 80; Best Local Similarity 77.0%; Score 516; DB 11; Length 119;
 Pred. No. 2. 32e-91; FT Non-Ter 119 119
 Mismatches 10; Indels 0; Gaps 0; FT Chain 20 >119
 FT Non-Ter 119 119
 SQ Sequence 119 AA: 13079 MW: 6B5A6578 CRC32;

Query Match 3 ELVLTOSPLSPVTPGEPASISCRSSQSLIHSNGNTLYLHWYLQKGQSPKLIIYKYSNRF 79
 Matches 80; Best Local Similarity 77.0%; Score 516; DB 11; Length 119;
 Pred. No. 2. 32e-91; FT Non-Ter 119 119
 Mismatches 10; Indels 0; Gaps 0; FT Chain 20 >119
 FT Non-Ter 119 119
 SQ Sequence 119 AA: 13079 MW: 6B5A6578 CRC32;

RESULT 3 PRELIMINARY:
 ID P97512 PRT: 249 AA.
 AC 01 MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DE SINGLE CHAIN FV ANTIBODY (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N. A.
 RL J. PLANT PHYSIOL. 144:427-429 (1994).
 RN [2]
 RP SEQUENCE FROM N. A.
 RX MEDLINE; 9608669.
 RA ARTSAIKO O., PEISKER M., ZUR NIEDEN U., FIEDLER U., WEILER E.W.,
 RA MUENTZ K., CONRAD U.,
 RL PLANT J. 8:745-750 (1995).
 DR EMBL; B29480; B283450; -.
 DR PFAM; PF00047; Ig.
 FT NON_TER 1 1
 FT NON_TER 249 249
 SQ SEQUENCE 249 AA: 26839 MW: 428B904E CRC32;

Query Match 3 DIELTQSPPSVVPGESVSSCRSSKSLLYSDGDSYLEFWLQRPGQSPQLIYRMSNLA 194
 Matches 80; Best Local Similarity 71.4%; Score 577; DB 11; Length 249;
 Pred. No. 6. 59e-108; FT Non-Ter 1 1
 Mismatches 14; Indels 0; Gaps 0; FT Signal 1 19
 FT Chain 20 >119
 FT Non-Ter 1 1
 SQ Sequence 249 AA: 26839 MW: 428B904E CRC32;

Query Match 3 DIELTQSPPSVVPGESVSSCRSSKSLLYSDGDSYLEFWLQRPGQSPQLIYRMSNLA 194
 Matches 80; Best Local Similarity 71.4%; Score 577; DB 11; Length 249;
 Pred. No. 6. 59e-108; FT Non-Ter 1 1
 Mismatches 14; Indels 0; Gaps 0; FT Signal 1 19
 FT Chain 20 >119
 FT Non-Ter 1 1
 SQ Sequence 249 AA: 26839 MW: 428B904E CRC32;

RESULT 4 PRELIMINARY:
 ID 055115 PRT: 119 AA.
 AC 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DE IG Kappa Chain (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N. A.

RESULT 5 PRELIMINARY:
 ID Q15535 PRT: 100 AA.
 AC 015535;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE V Kappa (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N. A.
 RA KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C.,
 RA TAKANO T.;
 RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DDJB DATA BANKS.
 DR EMBL; D90161; G1262585; -.
 DR PFAM; PF00047; Ig.
 FT NON_TER 1 1
 FT Non-Ter 100 100
 SQ SEQUENCE 100 AA: 10871 MW: 06A1440D CRC32;

Query Match 5 DIELTQSPPSVVPGESVSSCRSSKSLLYSDGDSYLEFWLQRPGQSPQLIYRMSNLA 194
 Matches 79; Best Local Similarity 79.0%; Score 512; DB 4; Length 100;
 Pred. No. 2. 07e-92; FT Non-Ter 1 1
 Mismatches 4; Indels 0; Gaps 0; FT Signal 1 19
 FT Chain 20 >119
 FT Non-Ter 1 1
 SQ Sequence 100 AA: 10871 MW: 06A1440D CRC32;

Query Match 5 DIELTQSPPSVVPGESVSSCRSSKSLLYSDGDSYLEFWLQRPGQSPQLIYRMSNLA 194
 Matches 79; Best Local Similarity 79.0%; Score 512; DB 4; Length 100;
 Pred. No. 2. 07e-92; FT Non-Ter 1 1
 Mismatches 4; Indels 0; Gaps 0; FT Signal 1 19
 FT Chain 20 >119
 FT Non-Ter 1 1
 SQ Sequence 100 AA: 10871 MW: 06A1440D CRC32;

RESULT 6 PRELIMINARY:
 ID 055116 PRT: 119 AA.
 AC 055116;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DE IG Kappa Chain (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N. A.

1 STRAIN-BALB/C; TISSUE-LIVER;
 2 MEDLINE: 87110625.
 3 CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;
 4 J. IMMUNOL. 138:932-938 (1987).
 5 EMBL; D00081; D1000494; -.
 6 NON_TER 119 119
 7 SEQUENCE 119 AA; 13117 MW; C201FBDB8 CRC32;

8 Query Match 62.3%; Score 505; DB 11; Length 119;
 9 Best Local Similarity 75.0%; Pred. No. 9.46e-91;
 10 Matches 75; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
 11

12 20 DLYMTQPLSLPVSLGDQASISCRSSQTLNSNTYLEWYLRKGPSQPLKLYKVSNRF 79
 13 1 DVMTQSPPLVLTGQPASISCRSSQSLHSSGNTYLNLQRPGQSFQPLIVLVSKE 60

14 80 SGYDREFSGSGSGTDFTLKIRISRYEAEDLGIVYCFQGSHP 119
 15 61 SGYDREFSGSGSGTDFTLKISGYEAEDLGIVYCFQGSHP 100

16 RESULT 7 PRELIMINARY; PRT; 119 AA.
 17 055117 PRELIMINARY; PRT; 119 AA.
 18 055117 PRELIMINARY; PRT; 119 AA.
 19 01-JUN-1998 (TREMBLREL. 06, CREATED)
 20 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 21 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 22 IG KAPPA CHAIN (FRAGMENT).
 23 MUS MUSCULUS (MOUSE).
 24 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 25 EUTHERIA; RODENTIA; RODENTIA; RODENTIA; RODENTIA.
 26 SEQUENCE FROM N.A.
 27 STRAIN-BALB/C; TISSUE-LIVER;
 28 CORBET S., MILILI M., FOUGEREAU M., SCHIFF C.;
 29 J. IMMUNOL. 138:932-938 (1987).
 30 EMBL; D00081; D1000494; -.
 31 NON_TER 119 119
 32 SEQUENCE 119 AA; 13117 MW; 7D3761A1 CRC32;

33 Query Match 62.0%; Score 502; DB 11; Length 119;
 34 Best Local Similarity 76.0%; Pred. No. 4.86e-90;
 35 Matches 76; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 36

37 20 DAVMTQPLSLPVSLGDQASISCRSSQTLNSNTYLEWYLRKGPSQPLKLYKVSNRF 79
 38 1 DVMTQSPPLVLTGQPASISCRSSQSLHSSGNTYLNLQRPGQSFQPLIVLVSKE 60

39 80 SGYDREFSGSGSGTDFTLKIRISRYEAEDLGIVYCFQGSHP 119
 40 61 SGYDREFSGSGSGTDFTLKISGYEAEDLGIVYCFQGSHP 100

41 RESULT 8 PRELIMINARY; PRT; 133 AA.
 42 061551 PRELIMINARY; PRT; 133 AA.
 43 01-NOV-1996 (TREMBLREL. 01, CREATED)
 44 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 45 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 46 CC49 FAB PRECURSOR (FRAGMENT).
 47 MUS MUSCULUS (MOUSE).
 48 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 49 EUTHERIA; RODENTIA.
 50 SEQUENCE FROM N.A.
 51 ABERGEL C., PADIAN E.-A., KASHMIRI S.V.S., MILENIC D., CALVO B.,
 52 SCHLOM J.;
 53 SUBMITTED (JUN-1992) TO EMBL/GENBANK/DDJB DATA BANKS.
 54 EMBL; M95574; G193215; -.
 55 PFAM; PF00047; 1g.

56 RESULT 9 PRELIMINARY; PRT; 115 AA.
 57 099826 PRELIMINARY; PRT; 115 AA.
 58 01-MAY-1997 (TREMBLREL. 03, CREATED)
 59 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 60 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 61 ANTI-HIV-1 GP120 V3 LOOP ANTIBODY DOI42-10 LIGHT CHAIN VARIABLE REGION
 62 DE (FRAGMENT).
 63 OS HOMO SAPIENS (HUMAN).
 64 OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 65 OC PRIMATES.
 66 RN [1].
 67 RP SEQUENCE FROM N.A.
 68 RA DITZEL H.J., PARREN P.W.H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
 69 RA BARBAS C.F., BURTON D.R.;
 70 RLM SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDJB DATA BANKS.
 71 DR EMBL; U82965; G180028; -.
 72 DR PFAM; PF00047; 1g.
 73 FT NON_TER 115 115
 74 SQ SEQUENCE 115 AA; 12740 MW; 745D103A CRC32;

75 Query Match 58.1%; Score 471; DB 4; Length 115;
 76 Best Local Similarity 60.0%; Pred. No. 1.03e-82;
 77 Matches 66; Conservative 23; Mismatches 20; Indels 1; Gaps 1.
 78

79 Db 4 LTQSPDSLAVSLGERATINCKSQTYFVNNSKKNLYWQRKGQSPPELLIWAESTRESG 63
 80 Qy 4 MTQSPPEPLVLTGQPASISCRSSQSLHSSGNTYLNLQRPGQSFQPLIVLVSKE 62

81 Db 64 VPDRFSSSGSGTDFTLKISLQADAVYCYQQYNNPFEGTGKVDFIK 113
 82 Qy 63 VPDRFSSSGSGTDFTLKISGYEAEDVGIVYCFQGSHP 112

83 RESULT 10 PRELIMINARY; PRT; 131 AA.
 84 099671 PRELIMINARY; PRT; 131 AA.
 85 01-MAY-1997 (TREMBLREL. 03, CREATED)
 86 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 87 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 88 DE MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
 89 OS HOMO SAPIENS (HUMAN).
 90 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 91 OC PRIMATES.
 92 RN [1].
 93 RP SEQUENCE FROM N.A.
 94 RA RYU C.J., JIN B.R., CHUNG H.K., HONG H.J.;
 95 RA SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDJB DATA BANKS.
 96 RLM EMBL; U66190; G1778126; -.
 97 DR PFAM; PF00047; 1g.
 98 RW SIGNAL.
 99 FT SIGNAL 1 22
 100 FT CHAIN 23 >131
 101 FT NON_TER 131
 102 FT POTENTIAL MONOCLONAL ANTIBODY KAPPA CHAIN VARIABLE REGION.

Db 59 TGPDRFGSGGTDFLTISLEPEDFATYCCQYSSRGVTFGQGTLEIK 111
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 61 SGVPDRFGSGGTDFLKISVEAEVGVYCMQFTHYP-YTFGQGTLEIK 112

RESULT 15
 ID Q99514 PRELIMINARY; PRT; 105 AA.
 AC Q99514;
 DT 01-MAY-1997 (TREMBLREL. 03 CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE LIGHT CHAIN FAB FRAGMENT (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBBJ DATA BANKS.
 DR EMBL; Y08118; E244854; -.
 DR PFAM; PF00047; ig.
 FT NON-TER 1 1
 FT NON-TER 105 105
 SQ SEQUENCE 105 AA; 11303 MW; 249B7EC3 CRC32;

Query Match 51.7%; Score 419; DB 4; Length 105;
 Best Local Similarity 60.0%; Pred. No. 1.58e-70; Gaps 2;

Matches 66; Conservative 17; Mismatches 22; Indels 5; Gaps 2;

Db 1 VMTQSPSSLSAVYGDRTVTICRASQSI-SS--YLNWYQQPKGKAPKLIVASSLQSG 55
 :|||||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Qy 3 VMTQSPSSLSVYLGOPASISCRSSQSLIHSSGNTYLNWLLQPGQSPOLIYVSKLESG 62

Db 56 VSRFSGSGSGDFTLTISSEPEDFATYCCQSYSPVTRQGTRLEIK 105
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 63 VPDFRGSGSGTDFLKISVEAEVGVYCMQFTHYP-YTFGQGTLEIK 112

Search completed: Thu Jan 14 17:11:35 1999
 Job time : 35 secs.

CC from the antibody Lo-CD2a, and the leader sequence from the LoCD2a gene.
 CC Lo-CD2a is produced by the cell line ARCC HB 11423. It is pref. a rat.
 CC monoclonal antibody and is produced using CD2. This antibody, or
 CC fragments of it, binds to all T lymphocytes and also to null cells but
 CC not to B lymphocytes. It binds to all CD4 and CD8 positive cells as
 CC defined by Leu3 and Leu2b antibodies respectively. Lo-CD2a can be used
 CC for inhibiting an immune response in a human patient, partic. an immune
 CC response mediated by T cell activation and proliferation resulting from
 CC graft-transplantation, graft-versus-host disease or autoimmune diseases.
 CC the missing residues are deduced from the DNA sequence given in the
 CC specification.
 Sequence - 253 AA;

Query Match 89.4%; Score 724; DB 11; Length 253;
 Best Local Similarity 87.5%; Pred. No. 5.86e-48;
 Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
 Sq

Db 142 dvl1tqppptllat1qgs1scrsqsl1hs5gntylnwllqrtgspaplylvskle 201
 Qy 1 DVMVQTQSPPPSLIVLGQPAS1CRSSQSLLHSSGNTYLNWLLQRPGQSPQLIVYVSKLE 60

Db 202 sgvphfsgsgsgtftlkisgvasedlgyycmftphytfagtktelk 253
 Qy 61 SGVPDRFSGSGSIDFTLKISGVAREDVGTYCNGFTHPYTFGGTKEIK 112

RESULT 2 standard; Protein: 134 AA.
 ID R59078; (first entry)
 AC R59078;
 DT 27-APR-1995
 KW LO-CD2a VL and signal peptide from MRC vector hcmy-villys-kr-neo.
 KW LO-CD2a: light; heavy; chain; variable; constant; antibody;
 KW signal sequence; MAC; vector; hcmy-villys-kr-neo; ARCC HB 11423;
 KW monoclonal antibody; MAB; T lymphocyte; null cell; B lymphocyte;
 KW CD4; CD8; Leu3a; Leu2b; inhibition; immune response; human;
 KW T cell; activation; proliferation; graft transplantation;
 KW graft-versus-host disease; autoimmune disease.
 OS Rattus rattus.
 Key
 FT peptide 1..22
 FT protein 23..134
 FT misc_difference 13
 FT misc_difference 15
 FT misc_difference 103
 FT misc_difference 105
 FT misc_difference 112
 FT misc_difference 128
 FT misc_difference 100
 PN W09420619.A.
 PT 15-SEP-1994.
 PT 04-MAR-1994; IB0043.
 PR 09-SEP-1993; US-027008.
 PA (UYLO) UNIV CATHOLIQUE LOUVAIN.
 PI Bazin H; Latinne D;
 DR WPI: 94-303026/37.
 DR N-PSDB; Q71875.

PT New anti-CD2 monoclonal antibody - used for inhibiting an immune response mediated by T cell activation and proliferation
 PS Claim 29; Fig 29A; 101pp; English.
 CC This sequence represents the LO-CD2a light chain variable region from
 CC the antibody LO-CD2a, and the signal sequence from the MRC vector hcmy-
 CC villys-kr-neo. LO-CD2a is produced by the cell line ARCC HB 11423. It
 CC is pref. a rat monoclonal antibody, and is produced using CD2. This

CC antibody, or fragments of it, binds to all T lymphocytes and also to
 CC null cells but not to B lymphocytes. It binds to all CD4 and CD8
 CC positive cells as defined by Leu3a and Leu2b antibodies respectively.
 CC LO-CD2a can be used for inhibiting an immune response in a human
 CC patient, partic. an immune response mediated by T cell activation
 CC and proliferation resulting from graft transplantation, graft-versus-
 CC host disease or autoimmune diseases.
 SQ Sequence 134 AA;

Query Match 87.9%; Score 712; DB 11; Length 134;
 Best Local Similarity 85.7%; Pred. No. 5.49e-47;
 Matches 9; Mismatches 7; Indels 0; Gaps 0;

Db 23 dg1tqppptllat1qgs1scrsqsl1hs5gntylnwllqrtgspaplylvskle 82
 Qy 1 DVMVQTQSPPPSLIVLGQPAS1CRSSQSLLHSSGNTYLNWLLQRGQSPQLIVYVSKLE 60

Db 83 sgvphfsgsgsgtftlkisgvasedlgyycmftphytfagtktelk 134
 Qy 61 SGVPDRFSGSGSIDFTLKISGVAREDVGTYCNGFTHPYTFGGTKEIK 112

RESULT 3 standard; Protein: 272 AA.
 ID W43913;
 AC W43913;
 DT 17-JUN-1998 (first entry)
 DE Mus musculus antibody specific for cyst nematode salivary protein.
 KW Cellulase activity; nematode; crop protection; parasitic;
 KW subventral oesophageal protein; cyst nematode;
 KW salivary protein.
 OS Mus musculus.
 Key
 FT Domain 1..112
 FT /note- "antibody variable domain light chain"
 FT Region 25..39
 FT /note- "Complementarity Determining Region"
 FT Region 55..61
 FT /note- "Complementarity Determining Region"
 FT Region 93..102
 FT /note- "Complementarity Determining Region"
 FT Peptide 113..127
 FT /note- "Gly-Ser peptide linker"
 FT Domain 128..273
 FT /note- "antibody variable domain heavy chain"
 FT Region 158..162
 FT /note- "Complementarity Determining Region"
 FT Region 529..579
 FT /note- "Complementarity Determining Region"
 FT Region 226..232
 FT /note- "Complementarity Determining Region"
 PN EP-818538-A1.
 PD 14-JAN-1988.
 PP 08-JUL-1986; 201890.
 PR 08-JUL-1986; EP-201890.
 PT Nematodal cellulase peptide(s) - useful as industrial cellulolytic
 enzymes or for plant protection
 Example; Pages 22-24; 28pp; English.
 PS The sequence is that encoding a peptide fragment of an antibody
 CC specific for a salivary protein of cyst nematodes. It can be used
 CC to help protect plants against parasitic nematodes.
 SQ Sequence 272 AA;

Query Match 78.8%; Score 638; DB 29; Length 272;
 Best Local Similarity 81.3%; Pred. No. 5.20e-41;
 Matches 9; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
 Db 1 dvymtqtptlsytqpassicssqslhsdgktyswlsqrqpskrlylvskld 60

RESULT	5	ID	W24989-standard; Protein; 135 AA.; ...
AC	W24989;	DE	Monoclonal antibody ZM1-1 (first entry)
DT	08-DEC-1997	DE	Heavy chain; light chain variable region; human; monoclonal antibody; immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic peripherial blood lymphocyte; surface antigen; cell culture; ion exchange chromatography; size separation; primer; PCR; Polymerase chain reaction; amplification; hybridoma; infection; immunosuppression; hepatitis; liver transplant.
KW	OS Homo sapiens.	Key	Location/Qualifiers
FT peptide	1..22	FT peptide	/note= "leader sequence"
FT protein	23..135	FT protein	/note= "mature protein"
FT region	23..122	FT region	/note= "VκII region"
FT domain	46..62	FT domain	/note= "complementarity determining region 1"
FT domain	77..83	FT domain	/note= "complementarity determining region 2"
FT domain	116..124	FT domain	/note= "complementarity determining region 3"
FT region	123..135	FT region	/note= "Jκ5 region"
FT PN	US5648077-A.	PN	15-TUL-1987.
PD	05-SEP-1986; 904517,	PF	05-SEP-1986; 904517,
PR	21-APR-1992; US-871426.	PR	05-SEP-1986; US-904517.
PR	31-OCT-1986; US-925196.	PR	11-MAY-1988; US-192754.
PR	15-JUN-1990; US-538796.	PR	27-JUN-1991; US-676036.
PR	14-JUN-1994; US-259372.	PR	06-JUN-1995; US-468861.
PA (SANO) SANDOZ LTD.	PI Ostberg LG;	DR	WPI; 97 372021/34.
PA	DR N-PSDB; IBS5843.	PT Treatment of hepatitis B - with human monoclonal antibody	Example 8; column 21-22; 25pp; English.
CC	This is the amino acid sequence of the light chain variable (V _L) region from the human monoclonal antibody (Mab) ZM1-1. The Mab was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating peripheral blood lymphocytes (PBL) and fusing them with a mouse/human xenogeneic cell line SP2/4. 5 cell lines were isolated: PEI-1, ZM1-1, ZM1-2, MD3-4 and LO-3. The cell lines were then tested for production of an anti-hepatitis B virus surface antigen antibody by ELISA. The Mabs are then purified from large scale cell culture by protein A chromatography, size separation on Sephadex S300 gel, and ion exchange chromatography on Q-Sepharose. The heavy and light chains of the Mabs were isolated and their amino acid sequences determined. Primers were generated and used to amplify cDNA synthesised from RNA purified from each hybridoma cell line. The sequences of the heavy and light chains (nucleic acid and amino acid) from Mabs PEI-1, ZM1-1, ZM1-2 and MD3-4 are shown in T85838-45 and W2984-91. The Mabs can be used to treat HBV infections in immunosuppressed patients or patients with chronic active hepatitis, especially liver transplant patients.	SQ Sequence 135 AA;	
Query Match	77..48;	Score	627; DB 24; Length 135;
Best Local Similarity	82..18;	Pred. No.	4 00e-40;
Matches	92; Conservative 7;	Mismatches	13; Indels 0; Gaps 0;
Db	23 dvrrtgspslsptlgqpastcrssls1vdsdgntylnwflqrpgassprriyqlsard 82		
Qy	1 dvrrtgspslsptlgqpastcrssls1vdsdgntylnwflqrpgassprriyqlsard 82		
Db	83 sgvpdrfsgsgstftlk1srreadvgyyccmqgthwplifgggttikleik 134		

Qy	61	SGVPDRFSGSGSGTDFTLKISSEADGVYTCMOTFHYPYTFGQQKLEIK 112
RESULT	6	
ID	R54052; standard; Protein; 135 AA.	
AC	R54052;	
DT	08-NOV-1994 (first entry)	
DE	Sequence of the VL region of monoclonal antibody ZM1-1 against hepatitis B virus surface antigen.	
DE	Hepatitis B virus; surface antigen.	
KW	monoclonal antibody; therapeutic.	
KW	HBSAG; diagnosis; HBV.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	region	1..22
FT		/label= leader
FT	region	23..122
FT		/label= VL II
FT	region	46..62
FT		/label= CDR 1
FT	region	77..83
FT		/label= CDR 2
FT	region	116..124
FT		/label= CDR 3
FT	region	123..135
FT		/label= CDR 4
FT	region	1..135
FT		/label= JL 5
PN	WO9411495-A.	
PD	26-MAY-1994	
PF	06-NOV-1992; 009749.	
PR	06-NOV-1992; WO-009749.	
PA	(SANDOZ LTD.	
PI	Ostberg LG;	
WPI	94-183497/22.	
DR	N-PSDB; Q64055.	
PT	Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus	
PS	Example; Page 41; 53pp; English.	
CC	Human volunteers were immunised with hepatitis B vaccine. MD3	
CC	2, ZM1-1 and PEI-1 hybridoma cell lines were derived from	
CC	lymphocytes of individuals immunised with Heptavax (Merck & Co).	
CC	Antibodies PEI-1, ZM1-1, M21-1, M21-2 and MD3-4 belong to the IgG1 class.	
CC	The cell lines producing PEI-1, ZM1-1 and ZM1-2 were deposited at ATCC HB923, 9191 and 9192 respectively. The cell lines all being typical (mouse x human) x human hybridomas and produce their respective Abs in conos. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable chains of Abs PEI-1, ZM1-1, ZM1-2 and MD3-4 were isolated and sequenced. Total RNA was extracted from 10(7) hybridoma cells of each cell line. ss DNA was synthesised using AMV-reverse transcriptase and oligo(dT) as primer. PCRs were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each positive clone after superinfection with ML3k07. Sequencing was by the dideoxy chain termination method (Sanger et al.).	
SQ	Sequence 135 AA;	
Query Match	77.4%	Score 627; DB 10; Length 135;
Best Local Similarity	82.1%	Pred. No. 4_00s-40;
Matches	92; Conservative	Mismatches 13; Indels 0;
Db	23 dvvtvttspispttgpasiscrssslvdsgdntylnwfqrgpsgrggttqylql	
Qy	1 DVVMIQSPPLVLTGPGASICRCSLLHSQNTLNLWLRQPGSPQPLYLVLV	
Db	83 sgvpdrfsgsgsgtfdflkisrveadgvyytcmtqgthwpltfggqrleik 134	
Qy	61 SGVPDRFSGSGSGTDFTLKISSEADGVYTCMOTFHYPYTFGQQKLEIK 112	
RESULT	7	
ID	W01525 standard; Protein; 135 AA.	
AC	W01525;	
DT	04-MAR-1997 (first entry)	
DE	Monoclonal antibody ZM1-1 light chain variable region	

(Note: this sequence does not appear in the specification and has been produced by modifying the given sequence of variant V-3225; Sequence 535 AA).

Query Match Score 627; DB 24; Length 535;
Best Local Similarity 79.5%; Pred. No. 4.00e-40;
Matches 89; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

o 134 dvimtqptltsvtigpasisckssqslldsdgktylnwllqrpgqspkrlyivskid 193
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
1 DVMNTQSPPSLVLGQASISCRSSQSLHSSNTYLNWLQRPGQSPQLIVSKLE 60

v 194 sgvprdfsgsgdftklnirveadlgvyycwggthspltgagtklelk 245
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
61 SGVPDRFSGSGSGTDFILKIGMCFTHYPYTFQGTTKLEIK 112

RESULT 9
W28491 standard; Protein: 535 AA.
W28491; 25-NOV-1997 (first entry)
Human P53 protein variant S-325 encoded by PEC176.
Leucine zipper domain; LZD; oligomerisation domain; mutant; mutant;
substitution; replacement; transactivation; viral protein VP16; HSV;
anti-oncogene; hyperproliferation; cancer; restenosis; SCFv;
Chimeric - Homo sapiens; single chain antibody variable domain.
Chimeric - Herpes simplex virus.
Synthetic.
WO9704092-A1.

CC W28491; 17-JUL-1996; F01111.
Human P53 protein variant S-325 encoded by PEC176.
Leucine zipper domain; LZD; oligomerisation domain; mutant; mutant;
substitution; replacement; transactivation; viral protein VP16; HSV;
anti-oncogene; hyperproliferation; cancer; restenosis; SCFv;
Chimeric - Homo sapiens; single chain antibody variable domain.
Chimeric - Herpes simplex virus.
Synthetic.
WO9704092-A1.

CC 06-FEB-1997.
CC 17-JUL-1996; F01111.
CC 19-JUL-1995; FR-008729.
CC (RHON) RHONE POULENC RORER SA.
CC Bracco L, Conseiller E;
CC WPI; 97-132633/12.
CC N-PSDB; T86221.
CC New P53 variants e.g. with oligomerisation domain replaced by
leucine zipper - useful for treating hyper-proliferative disorders,
SQ

ID R24710; standard; Protein: 112 AA.
AC R24710; (first entry)
DT 28-DEC-1992
DE Sequence of a chimeric anti-human fibrin antibody light chain
DE variable region contg. complementarity determining regions (CDRs)
DE A, B and C.
DE Chimeric monoclonal antibody; anti-fibrin antibody;
KW antithrombotic agent; myocardial infarction therapy.
OS Synthetic.
FT region 24..39
FT key /label= CDR A
FT region 55..61
FT /label= CDR B
FT region 94..101
FT /label= CDR C
EP-491351-A.
PN PD 24-JUN-1992; 121591.
PP 17-DEC-1990; 121591.
PR 18-DEC-1990; JP-413829.
PR 11-NOV-1991; JP-294464.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Iwasa S, Taka H, Watanabe T, Tada H;
WPI; 92-209528/26.
DR PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
PT Disclosure; Page 8; 87PP; English.
CC The inventors claim a chimeric monoclonal antibody which contains an
CC anti-human fibrin antibody light chain variable region contg. at
CC least one of the polypeptide chains A, B and C (R24704, R24705, R24706)
CC and a human antibody light chain constant region. A pref'd. chimeric
CC monoclonal antibody contains all three complementarity determining
CC regions. The chimeric Abs can be used both in vivo and in vitro
CC and, since they have very low immunogenicity as compared with mouse
CC Abs, they can be administered to humans for diagnostic and
CC therapeutic purposes. They are also more stable and show a longer
CC half-life in the blood as compared with the original mouse Abs.
SQ

Query Match	76.9%	Score 623; DB 5; Length 112;	Qy	61 SGVPDRFSGSGSGTDTLKISGVEAEQGVYXCMQFTHYPTFGQSTKLEIK 112
Best Local Similarity	78.6%	Pred. No. 8.40e-0;		
Matches	88; Conservative	9; Mismatches 15; Indels 0; Gaps 0;		
Db	1 dvmmaqtptltsvtiqgqafisctssqslldsdgktylnwlqrpgqspkrliylvskly 60	RESULT 12	ID R52057; standard; Protein; 113 AA.	
Qy	1 DVMVQSPSPSLVLTGQPASSICRSRSSLQHSSNTYLQRPGQSPQLIYLVSKL 60		AC R52057;	
Db	61 sgypdrftsgsgtaftlkirkirveedlgyycwggihfpytfggktleik 112		DT 10-OCT-1996 (first entry)	
Qy	61 SGVPDRFSGSGSGTDTLKISGVEAEQGVYXCMQFTHYPTFGQSTKLEIK 112		DE Light chain variable region of human KV2F antibody	
			KW antibody; humanised; murine; human; heavy chain; light; variable;	
			KW framework region; complementarity determining region; reshaping;	
			KW modelling; surface residue; modify.	
			OS Homo sapiens.	
		FH Key	Location/Qualifiers	
		FT region	1..23	
		FT /label= framework_region_1		
		FT /note= "FR 1"		
		FT region	24..39	
		FT /label= complementarity_determining_region_1		
		FT /note= "CDR 1"		
		FT region	40..54	
		FT /label= FR 2		
		FT region	55..61	
		FT /note= "CDR 2"		
		FT region	62..95	
		FT /label= FR 3		
		FT region	96..105	
		FT /note= "CDR 3"		
		PN EP-592106-A1.		
		PD 13-APR-1994.		
		PF 07-SEP-1993; 307051.		
		PR 09-SEP-1992; US-942245.		
		PA (PEDE/) PEDERSEN J T.		
		PA (IMMO) IMMUNOGEN INC.		
		PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;		
		DR WPI; 94-120230/15.		
		PT Method of resurfacing of rodent antibodies to produce humanised		
		PT antibody forms - for producing non-human antibodies with improved		
		PT therapeutic efficiency by presenting human surface on V-region		
		PS Example 1; Fig 4A; 230PP; English.		
		CC Modification of a rodent antibody (Ab) or fragment by resurfacing in		
		CC order to produce a humanised rodent Ab can be determined by calculating		
		CC homology between murine and human Ab antibody surfaces. In order to test		
		CC the resurfacing approach of the invention, three humanisation experiments		
		CC were set up: (1) traditional loop grafting; (2) resurfacing approach		
		CC using most similar chain; and (3) resurfacing approach using human		
		CC sequences with most similar surface residues. The Ab used was the murine		
		CC anti N901 Ab (see R52055). Experiment 2 was carried out using the present		
		CC sequence which represents the human KV2F Ab light chain variable region		
		CC with 87 percent homology with anti-N901 Ab. N901/KV2F (R52058) was prepd.		
		CC by CDR grafting.		
		SQ Sequence 113 AA;		
		Query Match 76.8%; Score 622; DB 18; Length 113;		
		Best Local Similarity 82.3%; Pred. No. 1.01e-39;		
		Matches 93; Conservative 7; Mismatches 12; Indels 1; Gaps 1;		
Db	1 dvvnmtqspislpvtlqqpasiscrssqslvsdntylnwfgqrpqgsprrliyksnrd 60	RESULT 13	ID W48248; standard; Protein; 112 AA.	
Qy	1 DVVNMTQSPPSLVLQGQPASTCRSSQSLHSSNTYLQRPGQSPQLIYLVSKL 60		AC W48248;	
Db	61 sgypdarfsqsgsgtdftlkirkirveadgvyycmqghwswtfggtkveik 113		DT 22-JUN-1998 (first entry)	
Qy	61 SGVPDRFSGSGSGTDTLKISG-VEADGVYXCMQFTHYPTFGQSTKLEIK 112		DE A77 anti-Fc alpha R antibody light chain variable kappa region.	
			KW A77 anti-Fc alpha R antibody; Fc-alpha receptor; antigen; cancer;	
			KW cytotoxic; white blood cell; infection.	
			OS Synthetic.	

OS Homo sapiens.
 PN W09802463-A1.
 PD 22-JAN-1998; U12013.
 PR 10-JUL-1997; U12013.
 PA (MEDAREX INC.
 PI DEO YM, Graziano R, Keler T;
 DR WPI; 98-11053/10.
 N-PSDB: V20501.
 PT Multispecific binding molecules reactive with Fc-alpha receptor and
 antigen - for treatment and prevention of cancer and infections by
 activating cytotoxic potential of Fc-alpha on white blood cells
 Claim 18; Page 60; 10pp; English.
 PS The present sequence represents A77 anti-Fc alpha R antibody light chain
 CC variable kappa region, which is used to produce the humanised
 CCC determinant in a bi-specific binding molecule of the present invention.
 CCC The present invention describes a bi- or multi-specific binding molecule
 CCC (1) comprising a first binding determinant (BD1) which binds a Fc alpha
 CCC receptor and a second BD (BD2) that binds to at least one antigen (Ag).
 CCC (1) are used: (i) to eliminate/reduce unwanted cells in a subject (human
 CC or animal); (ii) to vaccinate against pathogens (specifically Candida
 CC but many others disclosed including hepatitis and human immune
 CC deficiency viruses); (iii) to arm effector cells against pathogens or
 CC cancer cells. Ag may also be an allergen. (1) exploits the cytotoxic
 CC (cytolytic and phagocytic) potential of Fc alpha on white blood cells,
 CC improving their on cancer/infected cells. When used in vaccines, (1) may
 CC reduce the amount of antigen needed, and may be effective in patients
 CC who do not respond well to antigen.
 SQ Sequence 112 AA;

Query Match 76.5%; Score 620; DB 29; Length 112;
 Best Local Similarity 77.7%; Pred. No. 1.47e-39;
 Matches 87; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Db 1 digitqspltsitqgqasckssqslldsdgktyinwllqrgqgsprtriylyvskld 60
 Qy 1 DVMTQSPSLVTLGQASICRSSQSLLHSSNTYLNWLLQPGQSPQPLIYLYSRLK 60

Db 61 sgypdrfsgsggtodftlkisvreaedlglycwggahfpqtfggttkleik 112
 Qy 61 SGYDRESGSGSCDFTLKISVREAEDGVYTCMQLFTHYPTEFGQTKLEIK 112

RESULT 14
 ID R12361 standard; Protein: 132 AA.
 AC R12361.
 DT 15-AUG-1991 (first entry)
 DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.
 KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
 OS Mus musculus.
 PN W09107493-A.
 PD 13-NOV-1990; U06627.
 PR 13-NOV-1989; US-433703.
 PA (GREC) GREEN CROSS CORP.
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
 DR WPI; 91-17804/24.
 DR N-PSDB: Q12063.
 PT New chimeric mouse-human antibodies - used to detect, kill and
 PR remove HIV-1 antigen from sample
 PS Disclosure; fig 18; 107pp; English.
 This is the light (kappa) - chain variable (V) region of a mouse
 monoclonal antibody (Mab), 4D12, and is specific for an HIV-1
 viral antigen. It is used in the construction of a chimeric
 Mab comprising heavy and light chains having murine V regions
 and human C regions. The chimeric Mabs are more effective than
 murine Mab 4D12 since they have an increased compatibility in
 humans. The heavy and light chain V regions are joined by
 manipulating their respective joining (J) regions, to generate
 restriction enzyme recognition sites. The chimeric Mabs can be
 used as immunocoujugates, in association with e.g. toxins for HIV
 treatment. They can also be used in diagnosis of HIV.

CC See also Q12056-62.
 SQ Sequence.. 132 AA;

Query Match 76.3%; Score 618; DB 2; Length 132;
 Best Local Similarity 75.9%; Pred. No. 2.12e-39;
 Matches 85; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

Db 21 dvymtqptltsitqgqasckssqslldsdgktyinwllqrgqgsprtriylyvskld 80
 Qy 1 DVMTQSPSLVTLGQASICRSSQSLLHSSNTYLNWLLQPGQSPQPLIYLYSRLK 60

Db 81 sgypdrfsgsggtodftlkisvreaedgvycwggahfpqtfggttkleik 132
 Qy 61 SGYDRESGSGSCDFTLKISVREAEDGVYTCMQLFTHYPTEFGQTKLEIK 112

RESULT 15
 ID R12339 standard; Protein: 131 AA.
 AC R12339;
 DT 19-AUG-1991 (first entry)
 DE Mouse Mab 4D12 L chain V region.
 KW HIV-1; chimerica.
 OS Mus sp.
 PN W09107493-A.
 DR N-PSDB: Q12019.
 PT New chimeric mouse human antibodies - used in treatment, diagnosis
 and prophylaxis of HIV infections.
 PS Disclosure; fig 18; 107pp; English.
 CC The mouse VL gene product may be used to produce chimeric mouse
 human Abs against HIV-1 comprising human Ig constant regions and
 murine variable regions. These novel sequence are useful in
 treatment, diagnosis and prophylaxis of HIV infections, and may be
 produced by a bacterial, yeast or mammalian expression system.
 CC Sequence 131 AA;

Query Match 75.8%; Score 614; DB 2; Length 131;
 Best Local Similarity 76.6%; Pred. No. 4.45e-39;
 Matches 85; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Db 21 dvymtqptltsitqgqasckssqslldsdgktyinwllqrgqgsprtriylyvskld 80
 Qy 1 DVMTQSPSLVTLGQASICRSSQSLLHSSNTYLNWLLQPGQSPQPLIYLYSRLK 60

Db 81 sgypdrfsgsggtodftlkisvreaedgvycwggahfpqtfggttkleik 131
 Qy 61 SGYDRESGSGSCDFTLKISVREAEDGVYTCMQLFTHYPTEFGQTKLEIK 111

Search completed: Thu Jan 14 17:12:57 1999
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Title: Prescription:
>US-08-477-989B-93
(11-18) from US 08477989B.pdf

REFERENCE S48797
 #authors Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 #submission submitted to the EMBL Data Library, October 1994
 #description Molecular characterization of natural human anti-Sm autoantibodies.

#accession S49530
 #status preliminary
 #molecule_type mRNA
 ##residues 1-135 #label MAH
 ##cross-references EMBL:Z46348; NID:5560839; PID:9560840
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 FEATURE 34-17 #domain immunoglobulin homology #label IMM
 SUMMARY #length 135 #molecular-weight 14997 #checksum 8132

Query Match 76.3%; Score 653; DB 2; Length 135;
 Best Local Similarity 77.1%; Pred. No. 2.46e-80;
 Matches 91; Conservative 10; Mismatches 15; Indels 2; Gaps 1;

Db 20 QYOLVQSGAEEVKRPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNY 79
 Qy 1 QYOLVQSGAEEVKRPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNY 79
 Db 80 AQQKFGQRTMTDTSITSTAYMELSLRLSDDTAVYCCARATGY - NTWGQGTLYTVSS 135
 Qy 61 VVEREKKVYLTADESSSTAYMELSSLTSDTTAVYCCARAKFNYRFAYWGQGTLYTVSS 118

RESULT 3
 ENTRY D33548 #type complete
 TITLE 19 heavy chain V-1 region (WIL2) - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 17-Jan-1990 #sequence_revision 17-Jun-1990 #text_change
 16-Aug-1996

ACCESSIONS D33548
 REFERENCE A33548
 #authors Kripps, T.J.; Tonihave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
 Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
 #journal
 #title developmentally restricted immunoglobulin heavy chain
 variable region gene expressed at high frequency in chronic
 lymphocytic leukemia.
 #cross-references PMID:8345575
 #accession D33548
 #status preliminary; nucleic acid sequence not shown; not
 compared with conceptual translation

##molecule_type tRNA
 ##residues 1-123 #label KIP
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE 15-98 #domain immunoglobulin homology #label IMM
 SUMMARY #length 123 #molecular-weight 13789 #checksum 9208

Query Match 71.6%; Score 613; DB 2; Length 123;
 Best Local Similarity 73.2%; Pred. No. 4.25e-74;
 Matches 90; Conservative 11; Mismatches 17; Indels 5; Gaps 2;

Db 1 QYOLVQSGAEEVKRPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNY 60
 Qy 1 QYOLVQSGAEEVKRPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNY 60
 Db 61 AKEFKFGQRTMTDTSITSTAYMELSLRLSDDTAVYCCARASYCYYDCYYFFDTWQGTLYT 120
 Qy 61 VVEREKKVYLTADESSSTAYMELSSLTSDTTAVYCCARAKF--N-YRFAWQGQTLVT 115

Db 121 VSS 123
 Qy 116 VSS 118

RESULT 4
 ENTRY S55542 #type fragment

TITLE Ig heavy chain V region pe2 - mouse (fragment)
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
 08-Sep-1997

ACCESSIONS S55542
 REFERENCE Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 #authors Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
 #journal J. Mol. Biol. (1995) 247:932-946
 #title Comprehensive epitope analysis of monoclonal
 anti-protein/epitope antibodies using phage display libraries
 and synthetic peptides: revelation of antibody fine
 specificities caused by somatic mutations in the variable
 region genes.

#accession S55542
 #status preliminary
 #molecule_type mRNA
 ##residues 1-116 #label BOE
 ##cross-references EMBL:X82381; NID:9854302; PID:9854303
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE 14-97 #length 116 #checksum 418

Query Match 69.2%; Score 592; DB 2; Length 116;
 Best Local Similarity 70.1%; Pred. No. 7.80e-71;
 Matches 82; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

Db 1 VOLQSGAELVKPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNF 60
 Qy 2 VOLQSGAEVKKPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNF 61
 Db 61 EKFSSKATLTDVKSSTAVNQLSLSLTSDAVYCCTRGVVA - SVDYWGQGTLYTVSS 116
 Qy 62 EKFKKVYLTADESSSTAYMELSSLTSDTTAVYCCARGKENVRFAYWGQGTLYTVSS 118

RESULT 5
 ENTRY S20783 #type complete
 TITLE Ig heavy chain V region - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
 08-Sep-1997

ACCESSIONS S20783
 REFERENCE Mortari, F.; Wang, J.; Schroeder, H.W.
 #authors submitted to the EMBL Data Library, April 1992
 #description Analysis of human cord blood Ig heavy chain IgA and IgG
 repertoire.
 #accession S20783
 #status preliminary
 #molecule_type DNA
 ##residues 1-121 #label MOR
 ##cross-references EMBL:Z11957; NID:933899; PID:933900
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 121 #molecular-weight 13033 #checksum 8006

Query Match 68.2%; Score 584; DB 2; Length 121;
 Best Local Similarity 68.6%; Pred. No. 1.36e-69;
 Matches 83; Conservative 13; Mismatches 22; Indels 3; Gaps 2;

Db 1 QVQLVQSGAEVKPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNF 60
 Qy 1 QVQLVQSGAEVKPGASVKSCKSAGTFTGTYMMWVROAPGQGLEMWGWINPNSGGTNF 60
 Db 61 AOKLQGRATMRTDISTSTYMDLSGLRSRDTALYCARSGDTSPASIDYWGOGLTLYT 120
 Qy 61 VVEREKKVYLTADESSSTAYMELSSLTSDTTAVYCCARGKENVRFAYWGQGTLYT 115

Db 61 VVEREKKVYLTADESSSTAYMELSSLTSDTTAVYCCARGKENVRFAYWGQGTLYT 120
 Qy 61 VVEREKKVYLTADESSSTAYMELSSLTSDTTAVYCCARGKENVRFAYWGQGTLYT 117

Db 121 S 121
 Qy 118 S 118

#description Production of a Tobacco mosaic virus (TMV) inactivating neotop specific monoclonal antibody in Nicotiana tabacum.
#accession S25057
##molecule_type mRNA
##residues 1-474 ##label FIS
##cross-references EMBL:X67210; NID:954826; PID:954827
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY #length 474 #molecular-weight 52069 #checksum 4891

Query Match Score 582; DB 2; Length 474;
Best Local Similarity 67.2%; Pred. No. 2.78e-69;
Matches 80; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

Db 20 EVQLQSGPELVNNGASVKMSCKASGYFTTYVMHWVKPGQGLEWIGKINPNKGTRF 79
Qy 1 QYQLVQSGAEVKKGASVKSCASGYTTEYYMWVRQAPGQSELMRIDPDGSIDY 60

Db 80 NEERFKKATLTSKDKSSSTAYMELSSLTSDSAVYCARD-YDWFAYWQGTLYTVSA 137
Qy 61 VEKFKKVTLTADSSSTAYMELSSLTSDTAVYCARGFNT-RFAWQGTLYTVSS 118

RESULT 10
ENTRY PH1669 #type fragment
TITLE Ig heavy chain V region (clone 3B2) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change
ACCESSIONS PH1669
REFERENCES PH1642
#authors Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.
#journal J. Exp. Med. (1993) 178:331-336
#title The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A.
#accession PH1669
##molecule_type mRNA
##residues 1-110 ##label H1L
##experimental_source B Cell
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin heterotrimer; immunoglobulin
KEYWORDS 7-90
SUMMARY #length 110 #checksum 8449

Query Match Score 581; DB 2; Length 110;
Best Local Similarity 72.1%; Pred. No. 3.97e-69;
Matches 80; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Db 1 AEVKKPGASVKVSCKASGYFTGYMMHWVRQAPGQGLEWRINANGCTNYAOKFQGRV; 60
Qy 9 AEVKKPGASVKVSCKASGYTTEYYMWVRQAPGQGLEMRIDPDGSIDYVEKFKKV; 68

Db 61 TMTDRDSTITAYMELSLRSLSETDAVYCARDFLTGDAFDIWGQQTLYTVSS; 110
Qy 69 TLTDITSSSTAYMELLSLSDTAVYCARGFNT-RFAWQGTLYTVSS 118

RESULT 11
ENTRY C30560 #type fragment
TITLE Ig heavy chain V region (35.8.2H) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change
ACCESSIONS C30560
#authors Matsuda, T.; Kabat, E.A.
#journal J. Immunol. (1989) 142:863-870
#title Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.

#cross-references MUID:89110062
#accession C30560
##status preliminary
##molecule_type mRNA
##residues 1-118 ##label MAT
##cross-references GB:M24270; NID:9195615; PID:9195616
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin heterotrimer; immunoglobulin
KEYWORDS FEATURE 15-98
SUMMARY #length 118 #checksum 9448

Query Match Score 581; DB 2; Length 118;
Best Local Similarity 68.9%; Pred. No. 3.97e-69;
Matches 82; Conservative 16; Mismatches 19; Indels 2; Gaps 2;

Db 1 QVHLQSGAELVKPGASVKSCASGYFTPSYWMNWVKQRPQGOLEWIGEIDPNSNTNN 60
Qy 1 QVOLVQSGAEVKKGASVKSCASGYTTEYYMWVRQAPGQGLEMRIDPDGSIDY 60

Db 61 NQKFRNKATLTVDKSSNTAYMOLSSLTSESDAVYCARWT-GSWEAYWQGTLYTVSA 118
Qy 61 VEKFKKVTLTADSSSTAYMELSSLTSDTAVYCAR-GKFNRFAYWQGTLYTVSS 118

RESULT 12
ENTRY ...
TITLE ...
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS S31600
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougerousse, M.; Tonnelle, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
#accession S31600
##status preliminary
##molecule_type mRNA
##residues 1-136 ##label CUT
##cross-references EMBL:Z14165; NID:930994; PID:930995
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS FEATURE 34-117
SUMMARY #length 136 #checksum 9862

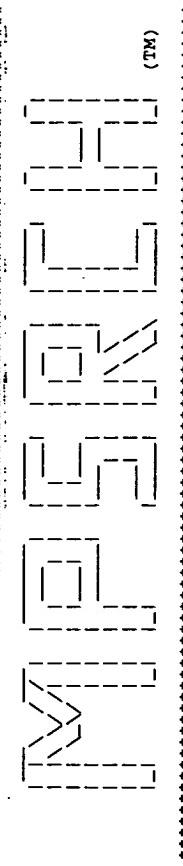
Query Match Score 580; DB 2; Length 136;
Best Local Similarity 70.3%; Pred. No. 5.67e-69;
Matches 83; Conservative 15; Mismatches 18; Indels 2; Gaps 2;

Db 20 QVQLVQSGAEVKKGASVKSCASGYFTPSYDINWVRQAPGQGLEMRIDPDGSIDY 79
Qy 1 QVOLVQSGAEVKKGASVKSCASGYTTEYYMWVRQAPGQGLEMRIDPDGSIDY 60

Db 80 AQKFQGRYMTNTSISTAYMELSSLRSLEDTAVYCARWRF-D-AFDIWGQQTLYTVSS 135
Qy 61 VEKFKKVTLTADSSSTAYMELSSLTSDTAVYCARGRFNRFAYWQGTLYTVSS 118

RESULT 13
ENTRY PH0962 #type fragment
TITLE Ig heavy chain V region (G6+ T-L42) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
ACCESSIONS PH0962
REFERENCE PH0952
#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.

#cross-references MUID:92202880
 #accession PH0912
 ##status nucleic acid sequence not shown
 ##molecule_type DNA
 ##residues 1-120 #label MAR
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE
 1-30 #region framework 1\\
 15-38 #domain immunoglobulin homology #label IMM\\
 31-35 #region complementarity-determining 1\\
 36-50 #region framework 2\\
 51-67 #region complementarity-determining 2\\
 68-88 #region framework 3\\
 99-108 #region complementarity-determining 3
 SUMMARY #length 120 #checksum 5559
 Query Match 67.6%; Score 579; DB 2; Length 120;
 Best Local Similarity 73.3%; Pred. No. 8.10e-69;
 Matches 88; Conservative 10; Mismatches 20; Indels 2; Gaps 1;
 #entry B227472 #type fragment.
 #label Ig heavy chain precursor V region (1E9) - mouse (fragment)
 #formal_name Mus musculus #common_name house mouse
 DATE 16-Aug-1998 #sequence_revision 16-Aug-1998 #text_change
 18-Oct-1996
 ACCESSIONS A27472
 REFERENCE
 #authors Liu, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
 #journal Gene (1987) 54:3-40
 #title Expression of mouse immunoglobulin heavy-chain cDNA in lymphoid cells.
 #cross-references MUID:8277430
 #accession A27472
 #molecule-type mRNA
 #residues 1-131 #label LIU
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE
 1-19 #domain signal sequence #status predicted #label SIG\\
 5-54 #region complementarity-determining 1\\
 20-111 #product Ig heavy chain V region 1E9 #status predicted
 #label MAB\\
 118-150 #domain immunoglobulin homology #label IMM\\
 34-117 #region complementarity-determining 2\\
 69-85 #region complementarity-determining 3\\
 118-125 #region complementarity-determining 3
 SUMMARY #length 131 #checksum 1501
 Query Match 67.4%; Score 577; DB 2; Length 131;
 Best Local Similarity 69.3%; Pred. No. 1.65e-68;
 Matches 79; Conservative 16; Mismatches 16; Indels 3; Gaps 3;
 Db 20 QVOLQQPQAELVKPGASVYKPSKASGTFTSYWVQAPQGLEMMGTPIFPANY 60
 Qy 1 QVOLQQPQAELVKPGASVYKPSKASGTFTSYWVQAPQGLEMMGTPIFPANY 60
 Db 61 ACKFQGRVTINADESTSTAYMELSSLRSEDTAVVYCARGGVAGRPHDYWGQGTLYVSS 120
 Qy 61 VEKFKKKVTLTADTSSTAYMELSSLRSEDTAVVYCARGGFNYR--FAYWGQGTLYVSS 118
 RESULT 14 B22769 #type complete.
 ENTRY B22769 #type complete.
 #label Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative
 sequence)
 #formal_name Mus musculus #common_name house mouse
 DATE 28-Dec-1987 #sequence_revision 28-dec-1987 #text_change
 16-Aug-1996
 ACCESSIONS A90911
 REFERENCE
 #authors Dildrop, R.; Bruggemann, M.; Radbrich, A.; Rajewsky, K.;
 Beyreuther, K.
 #journal EMBO J. (1982) 1:635-640
 #title Immunoglobulin V region variants in hybridoma cells. II.
 Recombination between V genes.
 #cross-references MUID:8423626
 #accession B22769
 #molecule_type protein
 #residues 1-120 #label DIL
 ##note the sequences of two spontaneously arising somatic
 variants, B1-8.V1 and B1-8.V2, appear to be identical;
 they differ from the B1-8 at 10 positions, most of
 which occur in the CDR2 region
 peptides and unsequenced residues were positioned by
 homology with the B1-8 sequence
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE
 15-98 #region domain immunoglobulin homology #label IMM
 SUMMARY #length 120 #molecular_weight 13465 #checksum 432
 Query Match 67.4%; Score 577; DB 2; Length 120;
 Best Local Similarity 68.3%; Pred. No. 1.65e-68;
 Matches 82; Conservative 13; Mismatches 23; Indels 2; Gaps 2;
 Db 1 QVOLQQPQAELVKPGASVYKPSKASGTFTSYWVQAPQGLEMMGTPIFPDSDTNY 60
 Qy 1 QVOLQQPQAELVKPGASVYKPSKASGTFTSYWVQAPQGLEMMGTPIFPDSDTNY 60
 Db 61 NKEFKGRATLTDKPSSTAYMELSSLTSSEDAVYCARGGTLYVSS 120
 Qy 61 VEKFKKKVTLTADTSSTAYMELSSLTSSEDAVYCARGGTLYVSS 118



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MPSearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jan 14 17:13:15 1999; Maspas time 5.76 Seconds

549.423 Million cell-updates/sec

Tabular output not generated.

Title: >US-08-477-989B-93

Descript: (1-18) from US08477989B.pep

Perfect Score: 856

Sequence: 1 QVQLVQSAEVKPGASVKV.....GKFNRYFAWGGTGLTVYSS 118

Scoring table: PAM 150

Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot35

1:swissprot

Statistics: Mean 42.127; Variance 73.640; scale 0.572

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID Description Pred. No.

Result No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	576	67.3	139	1	HV07	MOUSE	IG HEAVY CHAIN PRECURS	2.56e-103
2	571	66.7	118	1	HV11	MOUSE	IG HEAVY CHAIN V REGIO	3.66e-102
3	569	66.5	117	1	HV13	MOUSE	IG HEAVY CHAIN V REGIO	1.06e-101
4	568	66.4	138	1	HV48	MOUSE	IG HEAVY CHAIN PRECURS	1.8e-101
5	567	66.2	137	1	HV11	MOUSE	IG HEAVY CHAIN PRECURS	3.07e-101
6	566	66.1	117	1	HV1G	HUMAN	IG HEAVY CHAIN PRECURS	5.23e-101
7	565	66.0	117	1	HV1B	HUMAN	IG HEAVY CHAIN PRECURS	8.89e-101
8	556	65.0	117	1	HV12	MOUSE	IG HEAVY CHAIN V REGIO	1.06e-98
9	541	63.2	120	1	HV50	MOUSE	IG HEAVY CHAIN V REGIO	3.00e-95
10	539	63.0	140	1	HV02	MOUSE	IG HEAVY CHAIN PRECURS	8.66e-95
11	521	60.9	117	1	HV09	MOUSE	IG HEAVY CHAIN PRECURS	1.18e-90
12	520	60.7	120	1	HV03	MOUSE	IG HEAVY CHAIN PRECURS	1.99e-90
13	513	59.9	117	1	HV04	MOUSE	IG HEAVY CHAIN PRECURS	8.00e-89
14	511	59.0	117	1	HV06	MOUSE	IG HEAVY CHAIN PRECURS	2.30e-88
15	505	59.0	117	1	HV10	MOUSE	IG HEAVY CHAIN PRECURS	5.41e-87
16	503	58.8	114	1	HV00	MOUSE	IG HEAVY CHAIN V REGIO	1.55e-86
17	500	58.8	143	1	HV1C	HUMAN	IG HEAVY CHAIN PRECURS	1.55e-86
18	499	58.4	117	1	HV49	MOUSE	IG HEAVY CHAIN PRECURS	7.52e-86
19	490	57.2	136	1	HV15	MOUSE	IG HEAVY CHAIN PRECURS	1.44e-83
20	489	57.1	117	1	HV05	MOUSE	IG HEAVY CHAIN PRECURS	2.44e-83
21	487	56.9	117	1	HV52	MOUSE	IG HEAVY CHAIN PRECURS	6.96e-83
22	484	56.5	117	1	HV14	MOUSE	IG HEAVY CHAIN PRECURS	3.36e-82
23	480	56.1	121	1	HV01	MOUSE	IG HEAVY CHAIN V REGIO	2.74e-81

ALIGNMENTS

RESULT ID	HV07	MOUSE	STANDARD;	PRT;	139 AA.
AC P01751; P01752;					
DT 21-JUL-1986 (REL. 01, CREATED)					
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)					
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)					
DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186/2).					
OS MUS MUSCULUS (MOUSE).					
OC EUKARYOTA; MELAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC EUTHERIA; RODENTIA.					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=C57BL/6;					
RX MEDLINE; 81230548.					
RA BOTHMELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJENSKY K., BALTIMORE D.;					
RL CELL 24:625-637 (1981).					
CC -1- THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEM (4-HYDROXY-3-NITROPHENYL)ACETYL (NPA) ANTIBODIES.					
CC CC					
CC ANTIODIES TO THE HAPTEM (4-HYDROXY-3-NITROPHENYL)ACETYL (NPA) ANTIBODIES.					
CC DR EMBL; J00529; G195115; -.					
DR PIR; A0204; MHMS18.					
DR HSSP; P01810; LJHL.					
KW IMMUNOGLOBULIN V REGION; SIGNAL.					
FT SIGNAL	1	19			
FT CHAIN	20	139			
FT DOMAIN	20	139			
FT DOMAIN	50	54			
FT DOMAIN	55	68			
FT DOMAIN	69	85			
FT DOMAIN	86	117			
FT DOMAIN	118	124	D SEGMENT,		
FT DOMAIN	125	139	JH2 SEGMENT.		
FT DISULFID	41	115	BY SIMILARITY.		
FT NON-TER	139	139			
SQ SEQUENCE	139	139 AA;	15419 MW; DEBB2C7DA CRC32;		
Query Match 67 3%; Score 576; DB 1; Length 139;					
Best Local Similarity 68 1%; Pred. No. 2.56e-103;					
Matches 82; Conservative 14; Mismatches 22; Indexes 2; Gaps 2;					
Db 20 QVQLQQPQGELVKAGASVKSCKASGYTTSYWMHWKQRPGRGLEWIGRIDPNGGTKY 79					
Qy 1 QVQLVQSGNEVKKGASVKSCKASGYTTSYWMHWKQRPGRGLEWIGRIDPNGGTKY 79					
Db 80 NEKFKSATLTVDKPSSATYMQLSSLTSEDASYYCARYDYGGSSYFYDWQGTTLTVSS 139					

Qy 61 VEKKKKVTLADTSSTAYMELSSLTSDTAVYCAR-GRENRY-FAYWGGTLYTVSS 118
 ...
 RESULT 2 STANDARD; PRT; 118 AA.
 ID HV51-MOUSE
 AC P06370;
 DT 01-JAN-1988 (REL. 05, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
 DE MUS MUSCULUS (MOUSE).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 84182519.
 RL DILDROP R., BOYENS J., SIEKEVITZ M., BEYREUTHER K., RAJEWSKY K.;
 RL EMBO J. 3:517-523 (1984).
 DR PIR; A02040; MMNS38.
 DR HSSP; P01772; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 99 104 D SEGMENT.
 FT DOMAIN 105 118 J SEGMENT.
 FT DISUFLID 22 96 BY SIMILARITY.
 FT NON_TER 118 118 AA; 12934 MW; 2D1DC677 CRC32;
 SQ SEQUENCE 118 AA; 12934 MW; 2D1DC677 CRC32;

Query Match 66.7% Score 571; DB 1; Length 118;
 Best Local Similarity 64.7%; Pred. No. 3.66e-102;
 Matches 77; Conservative 19; Mismatches 21; Indels 2; Gaps 2;

Db 1 EVQLQOSGPPEVKPGASVKISSCKASGYTFDYYMWKQSHGKSLIEWIGDINPNNGGTSY 60
 Qy 1 QVQLYQSGAEVKPGASVKISSCKASGYTFEYYMWQAPGQGLFEMGRIDPEDSIDY 60
 Db 61 NQKFQKATLTVKDSSATYCARSLTSEDAVYCAR-GYDPEFDVNGTGTLYTVSS 118
 Qy 61 VEKKKKVTLADTSSTAYMELSSLTSDTAVYCAR-GRENRY-FAYWGGTLYTVSS 118
 ...
 RESULT 3 STANDARD; PRT; 117 AA.
 ID HV13-MOUSE
 AC P01757;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 CC -1- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
 CC THE D AND J SEGMENTS.
 CC -1- THIS PROTEIN BINDS DEXTRAN.
 DR PIR; A26242; MMNS35.
 DR HSSP; P01789; 2EGW.
 KW IMMUNOGLOBULIN V REGION.
 FT DISUFLID 22 96 BY SIMILARITY.
 FT NON_TER 117 117 AA; 13024 MW; E7548A05 CRC32;

Query Match 66.5% Score 569; DB 1; Length 117;
 Best Local Similarity 65.3%; Pred. No. 1.06e-101;
 Matches 77; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

Db 1 EVQLQOSGPPEVKPGASVKISSCKASGYTFDYYMWKQSHGKSLIEWIGDINPNNGGTSY 60
 Qy 1 QVQLYQSGAEVKPGASVKISSCKASGYTFEYYMWQAPGQGLFEMGRIDPEDSIDY 60
 ...
 Query Match 66.4% Score 568; DB 1; Length 138;
 Best Local Similarity 66.4%; Pred. No. 1.81e-01;
 Matches 79; Conservative 18; Mismatches 21; Indels 1; Gaps 1;

Db 20 QVQLQGPQGAEVKPGASVKISSCKASGYTFDYYMWKQPGQGLEWIGEINPNDGRSY 79
 Qy 1 QVQLYQSGAEVKPGASVKISSCKASGYTFEYYMWQAPGQGLFEMGRIDPEDSIDY 60
 Db 80 NEKFNKATLTVKDSSATYCARSLTSEDAVYCAR-GYDPEFDVNGTGTLYTVFA 138
 Qy 61 VEKKKKVTLADTSSTAYMELSSLTSDTAVYCAR-GRENRY-FAYWGGTLYTVSS 118
 ...
 RESULT 5 STANDARD; PRT; 137 AA.
 ID HV11-MOUSE
 AC P01755;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 CC -1- THE GAMMA-2A CHAIN mRNA WAS CLONED FROM A HYBRIDOMA MAKING
 CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
 CC -1- THE GAMMA-2A CHAIN mRNA WAS CLONED FROM A HYBRIDOMA MAKING
 DR PIR; J00339; G195119; -
 DR EMBL; J00339; G195119; -
 DR PIR; A02038; G2MS43.

FT	NON_TER	120	120 MW;	BBABCCLL-CRC32;			
SQ	SEQUENCE	120 AA;	13307 MW;				
Query Match	Score 520; DB 1; Length 120;	Pred. No. 1.99e-90; 18; Mismatches 22; Indels 3; Gaps 1;					
Best Local Similarity 64.2%; Matches 77; Conservative							
Db	1 VQLQGSQAEYLRYAGSSVYKMSCKASGTYFTSYGINWYKQRPGGLEWIGNGTYKVN 60						
Qy	2 VQLVQSGAEVKPGASTKVSCKASGTFTEYMWWRQAPGGLEMRIDPEDSDIVY 61						
Db	61 EFKGKTTLTVDKSSSTAYMRLSLTSEDSAVFCARSVYGGSYFDDYNGQGTITVSS 120						
Qy	62 EFKKKVTLTADTSSTAYMELLSSTDDTAVYCARKE--NYRFAYWGGLTVVSS 118						
RESULT 13	STANDARD; PRT; 117 AA.						
ID	HV04_MOUSE						
AC	P01748; 01, CREATED)						
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)						
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)						
DE	IG HEAVY CHAIN PRECURSOR V REGION (23).						
OS	MUS MUSCULUS (MOUSE).						
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=C57BL/6;						
RX	MEDLINE; 8123548.						
RA	BALTIMORE D.						
RA	BALTIMORE A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,						
RA	CELL 24:625-637(1981).						
CC	- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.						
DR	PIR; A02030; HVMS23.						
DR	IMMUNOGLOBULIN V REGION; SIGNAL.						
FT	SIGNAL 1 19						
FT	CHAIN 20 117	IG HEAVY CHAIN V REGION (23).					
FT	DOMAIN 20 49	FRAMEWORK 1.					
FT	DOMAIN 50 54	COMPLEMENTARITY-DETERMINING 1.					
FT	DOMAIN 55 68	FRAMEWORK 2.					
FT	DOMAIN 69 85	COMPLEMENTARITY-DETERMINING 2.					
FT	DOMAIN 86 117	FRAMEWORK 3.					
FT	DISULFID 41 117	BY SIMILARITY.					
FT	NON_TER 117 117						
SQ	SEQUENCE 117 AA; 12772 MW; 66B3D1A CRC32;						
Query Match	Score 513; DB 1; Length 117;	Pred. No. 8.00e-89; 13; Mismatches 15; Indels 0; Gaps 0;					
Best Local Similarity 71.4%; Matches 70; Conservative							
Db	20 QVLOQGPGETLVKGASVKLCKASGTYFTSYWMHWYKQRPGGLEIGNPNGCTNY 79						
Qy	1 QVLYQSGAETYKPGASVKSCKASGTYFTTEYMWWRQAPGGLEMRIDPEDSDIVY 60						
Db	80 NEKFKRVTLTVDKSSSTAYMELLSSTDDTAVYCAR 117						
Qy	61 VEKFKKVTLTADTSSTAYMELLSSTDDTAVYCAR 98						
RESULT 14	STANDARD; PRT; 117 AA.						
ID	HV06_MOUSE						
AC	P01750; 01, CREATED)						
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)						
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)						
DE	IG HEAVY CHAIN PRECURSOR V REGION (102).						
OS	MUS MUSCULUS (MOUSE).						
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=C57BL/6;						
RX	MEDLINE; 8124548.						
RA	BALTIMORE D.						
RA	BALTIMORE A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,						
RA	CELL 24:625-637(1981).						
CC	- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.						
DR	PIR; C03034; HVMS45.						
DR	IMMUNOGLOBULIN V REGION; SIGNAL.						
FT	SIGNAL 1 19	IG HEAVY CHAIN V REGION (145).					
FT	CHAIN 20 117	FRAMEWORK 1.					
FT	DOMAIN 20 49	COMPLEMENTARITY-DETERMINING 1.					
FT	DOMAIN 50 54	FRAMEWORK 2.					
FT	DOMAIN 55 68	COMPLEMENTARITY-DETERMINING 2.					
FT	NON_TER 117 117	BY SIMILARITY.					
SQ	SEQUENCE 117 AA; 12921 MW; D9E6B000 CRC32;						
Query Match	Score 505; DB 1; Length 117;	Pred. No. 5.4e-87; 12; Mismatches 16; Indels 0; Gaps 0;					
Best Local Similarity 71.4%; Matches 70; Conservative							
Db	20 QVOLQQPAAEVKPGASVKSCKASGTYFTSYWMHWYKQRPGGLEIWTYYMWWRQAPGGLEMRIDPEDSDIVY 79						

QY 1 QYOLYQSGAEVKPGASVKYSCRASGYTEYTMWVRQAPGQGLELMGRIDPDGSDY 60
DB 80 NEERFSKAVLTVDPESSAYMQQSSLTSEDSAVYCAR 117
QY 61 VEKEFKKVTLTADTSSRAYMELSSLTSDTAVYCAR 98

Search completed: Thu Jan 14 17:13:28 1999
Job time : 13 secs.

RA GILKESON G.S.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBBJ DATA BANKS.
 DR EMBL; US5154; G1389780;
 DR PFAM; PF00047; ig.
 FT NON-TER 1
 FT NON-TER 123
 SQ SEQUENCE 123 AA; 13806 MW; DA290D89 CRC32;

Query Match Score 61.4%; Length 123;
 Best Local Similarity 61.8%; Pred. No. 2.50e-88;
 Matches 76; Conservative 19; Mismatches 23; Indels 5; Gaps 4;

Db 1 EIQOLQSGATELVKGASVYKISKASGYSFTGYNANWVKOSHGSLEWGDINPYGGTRY 60
 QY 1 QVQLVQSGAEVKKGASVYKKGASVYKSGASGYTEYIMWVRQAPGQOLEMGRIPDGSDIDY 60

Db 61 SQKEFDKATLTDKSSRTAYMQLNLSLTSDDSAVYCARDYTYYTYDEGCFAYNGQGTLYT 120
 QY 61 VEKEFKKVTLTADTSSTAYMELSSLTSDTAVYCARG-KF-NY-R-FAYNGQGTLYT 115

Db 121 VSA 123
 QY 116 VSS 118

RESULT 11
 ID P97512 PRELIMINARY; PRT; 249 AA.
 AC P97512;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DT SINGLE CHAIN FV ANTIBODY (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ARTAENKO O., WELLER E.W., MUENTZ K., CONRAD U.;
 RL J. PLANT PHYSIOL. 144:427-429(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RW MEDLINE; 608609.
 RA ARTAENKO O., PEISKER M., ZUR NIEDEN U., FIEDLER U., WELLER E.W.,
 RA MUENTZ K., CONRAD U.;
 RL PLANT J. 8:745-750(1995).
 DR PFAM; PF00047; ig.
 FT NON-TER 1
 FT NON-TER 249
 SQ SEQUENCE 249 AA; 26839 MW; 428B904E CRC32;

Query Match Score 61.4%; Length 249;
 Best Local Similarity 63.0%; Pred. No. 2.50e-88;
 Matches 75; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

Db 1 QVOLQSGATELVKGASVYKISKASGYSFTGYNANWVKOSHGSLEWGDINPYGGTRY 60
 QY 1 QVQLVQSGAEVKKGASVYKKGASVYKSGASGYTEYIMWVRQAPGQOLEMGRIPDGSDIDY 60

Db 61 VPREQDQATITADTSSTAYMELSSLTSDTAVYCARG-KF-NY-R-FAYNGQGTLYT 119
 QY 61 VEKEFKKVTLTADTSSTAYMELSSLTSDTAVYCARG-KF-NY-R-FAYNGQGTLYT 118

RESULT 12
 ID P97746 PRELIMINARY; PRT; 120 AA.
 AC P97746;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE MONOCLONAL ANTIBODY 1D11 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

RESULT 13
 ID 035529 PRELIMINARY; PRT; 116 AA.
 AC 035529;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE ANTI-ACID PHOSPHATASE VARIABLE HEAVY CHAIN 18 (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA TAKATA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.,
 RA HATANO S.;
 RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBBJ DATA BANKS.
 DR D50137; D1024480; -.
 DR PFAM; PF00047; ig.
 FT NON-TER 1
 FT NON-TER 116
 SQ SEQUENCE 116 AA; 13097 MW; BFF6E1A CRC32;

Query Match Score 59.0%; Length 116;
 Best Local Similarity 61.0%; Pred. No. 3.0e-85;
 Matches 72; Conservative 19; Mismatches 25; Indels 2; Gaps 1;

Db 1 QLKQESGEGLVKGASVYKISKASGYSFTGYNANWVKOSHGSLEWGDINPYGGTRY 60.
 QY 1 QVQLVQSGAEVKKGASVYKKGASVYKSGASGYTEYIMWVRQAPGQOLEMGRIPDGSDIDY 60

Db 61 NQFKDKASLTVDKSSSTAYMELSSLTSDTAVYCARG-KF-NY-R-FAYNGQGTLYT 116
 QY 61 VEKFKKVTLTADTSSTAYMELSSLTSDTAVYCARG-KF-NY-R-FAYNGQGTLYT 118

RESULT 14
 ID P97771 PRELIMINARY; PRT; 241 AA.
 AC P97771;
 DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
 DE ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUKARYOTA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHUNG J.-H., LEE S.D., YI K.S., SUH S.H., CHOI S.J., KIM H.J.,

RA KIM I.J., CHOI I.H., CHUNG H.K.;
 RLU SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ. DATA BANKS.
 DR EMBL; U88067; G1350548; -
 DR PFAM; PF00047; 19.
 FT NON-TER 1 1
 FT NON-TER 241 241
 SQ SEQUENCE 241 AA; 26086 MW; EBB2D29D CRC32;

Query Match 59.2%; Score 507; DB 11; Length 241;
 Best Local Similarity 56.3%; Pred. No. 3.78e-84;
 Matches 67; Conservative 24; Mismatches 26; Indels 2; Gaps 2;

Db 1 QVKLQQSGPEELAKPGTETVKISCKASGTYFTDGMNWKQAPGKGLKWMGWINTYTGEPY 60
 Qy 1 QVLYQSGAEVKPGASVKVSCKASGTYFTEVYMWYRQAPOQGLELMGRIDPEDGSTDY 60

Db 61 ADDFKGRFAFSLETSASTAYLQINNLKEDTATYFCARKDLRLY-FDYWGQGTYYTVSS 11.8

Qy 61 VEKFKKVTLADTSSTAYMELSSLSDDTAVIYCARGF-NYRFAYWGQGTLYTVSS 11.8

RESULT 15
 ID 055113 PRELIMINARY; PRT; 98 AA.
 AC 055113;
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE A6 ANT-1 [4-HYDROXY-3-NITROPHENYL (PHENOLATE FORM)] ACETYL MAB V-H
 DE REGION (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EURYOTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE; 88198051.

RA SOBANORIO A.; ADOMA T.; HAMADA Y.; SAKATO N.; FUJIO H.;
 RL J. BIOCHEM. 102:1337-1343 (1987).
 DR EMBL; D00233; D1019624; -
 FT NON-TER 1 1
 FT NON-TER 98 98
 SQ SEQUENCE 98 AA; 10865 MW; 4C615AE9 CRC32;

Query Match 58.9%; Score 504; DB 11; Length 98;
 Best Local Similarity 71.1%; Pred. No. 1.72e-83;
 Matches 69; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Db 1 QVLOQXGAELAKPGASVKSLCKASGTYFTSTWMHWYKQRPGRLEGIRDPNSGGTKY 60
 Qy 1 QVLYQSGAEVKPGASVKVSCKASGTYFTEVYMWYRQAPOQGLELMGRIDPEDGSTDY 60

Db 61 NEFKSTATLTVDKPSSTAYMQLSSLAESDASYYCA 97

Qy 61 VEKFKKVTLADTSSTAYMELSSLSDDTAVIYCARGF-NYRFAYWGQGTLYTVSS 97

Search completed: Thu Jan 14 17:14:12 1999
 Job time : 25 secs.

RESULT	4	W22418 standard; Protein; 116 AA.
ID	W22418;	
AC	W22418;	
DE	08 DEC-1997 (first entry)	
DE	Reshaped human AUK12-20 VH	
KW	Alpha-4 integrin; humanised antibody	
KW	asthma; atherosclerosis; AIDS; de	
KW	metastasis; inflammatory bowel dis	
KW	transplant rejection; graft versus	
KW	atopic dermatitis; psoriasis; myo-	
KW	acute leukaocyte mediated lung inj	

RESULT³
R7491 standard; Protein; 120 MA.
R7491:
AC AC
DT DT
DE DE
JUL-1994 (first entry)
Humanized anti-CD18 AB 60.3 heavy chain.

OS	Chimeric synthetic.
FH	Location/Qualifiers
Key	1..30
region	/label= FRI
FT	31..35
FT	/label= CDR1
region	
FT	
FT	

region 36..49 /label= FR2
 region 50..66 /label= CDR2
 region 67..98 /label= CDR3
 region 99..105 /label= CDR3
 region 106..116 /label= FR4
 PN WO9718838-A1.
 PD 29 MAY-1997.
 PF 21-NOV-1996; U18807.
 PR 21-NOV-1995; US-1995-21.
 (ATHENE-) ATHENA NEUROSCIENCES INC.
 PPI Bendig NM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
 WPI: 97-2978/97.
 DR Uses of humanised alpha-4 integrin antibody - for treatment of
 asthma, atherosclerosis, AIDS, dementia, etc.
 Example 6: Page 44; 107Bp; English.
 This polypeptide comprises version 'b', of a reshaped human
 antibody AUKL2-20 VH region. A DNA fragment encoding the
 polypeptide was subcloned into vector pUC19 for use as a template
 for PCR amplification and production of version 'a', of a reshaped
 human 21.6 VH region (see W22413) that can be used in the
 construction of novel humanised anti-alpha-4 integrin antibodies.
 Claimed humanised antibodies are useful in the treatment of
 asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
 bowel disease, rheumatoid arthritis, transplant rejection, graft
 versus host disease, tumour metastasis, nephritis, atopic
 dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
 mediated lung injury.
 Sequence 116 AA;
 SQ

determining regions

PS Disclosure: Page 157-8; 207pp; Japanese.

CC The sequences given in R29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which caused the production of the antibody from the hybridoma cell line. Sequence 135 AA;

Query Match 7 Score 653; DB 6; Length 135;

Best Local Similarity 79.7%; Pred. No. 2.35e-41; Indels 2; Gaps 2; Matches 94; Conservative

Db 20 qvglyqsgaevikkgasvksckasgstsyyihwrgapgglewgyidpfngtsty 79

Qy 1 QVQLVQSGAEVKKGASVKSCKASGSTSYYIHWRGAPGGLEWMGRIDPSEGSDY 60

Db 80 nqkfkgkvmtvdstnctaymellssldtaayccargg-n-nrfayyqgqtlytvss 135

Qy 61 VEKEFKKVTLTADTSSTAYMELSSLTDDTAVYYCARSKENFTRAYNGQQGLTVYVSS 118

RESULT ID W27551 standard; protein; 120 AA.
AC W27551
DT 23-JAN-1998 (first entry)
DE Human. Ab heavy chain variable region VH1B consensus.
KW Human; antibody; preparation; library; VH1B; variable region;
KW heavy chain; consensus.
OS Homo sapiens.
PN W09/08322-A1.
PD 06-MAR-1997.
PF 19-AUG-1996; E03647.
PR 19-AUG-1995; EP-11-13021.
PA (MOPR) MORPHOYS GES PROTEINOPTIMIERUNG MBH.
PI Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
DR N-PSDB; T87949.
PT Preparation of human derived antibody gene library - using synthetic
consensus sequences, and signal consensus antibody gene as universal
framework for highly diverse antibody libraries
PS Example 1; Fig 5B; 436pp; English.
CC The present sequence is the human antibody heavy chain
variable region synthetic sequence VH1B, used in the preparation of
a human derived antibody gene library.
SQ Sequence 120 AA;

Query Match 7 Score 648; DB 25; Length 120;

Best Local Similarity 76.7%; Pred. No. 5.86e-41; Indels 2; Gaps 1; Matches 92; Conservative

Db 1 qvglyqsgaevikkgasvksckasgstsyyihwrgapgglewgyidpfngtsty 60

Qy 1 QVQLVQSGAEVKKGASVKSCKASGSTSYYIHWRGAPGGLEWMGRIDPSEGSDY 60

Db 61 agkfqgrvmtrdtsistaymellssldtaayccarggdifyandywggtlytvss 120

Qy 61 VEKEFKKVTLTADTSSTAYMELSSLTDDTAVYYCAR-GKENVRFAYWGQTLTVYVSS 118

PT	region	45..54	/label= CDR1
CC	region	69..85	/label= CDR2
CC	region	118..128	/label= CDR3
CC	EP-534742-A.		
CC	PD 31-MAR-1993.		
CC	PF 24-SEP-1992; 308680.		
CC	PF 26-SEP-1991; GB-020467.		
CC	PA (CLLT) CELITECH LTD.		
CC	PI Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;		
CC	PI Menendez AT, Owens RJ;		
CC	DR WPI: 93-102837/13.		
CC	DR N-PSDB; Q38882-89.		
CC	PT Anti-human milk fat globule humanised antibodies - useful as conjugate for in-vivo diagnosis and therapy of e.g. ovarian or breast cancer		
CC	PT Disclosure; Page 27; 57pp; English.		
CC	PS This sequence represents the CDR grafted heavy chain, gH1. This protein is encoded by the DNA constructed using the oligonucleotides given in Q38882-89. This heavy chain was used in conjunction with a light chain (see also R33954) in the production of a humanised antibody molecule (HAM). At least one of the complementarity determining regions (CDR's) of the variable domain is derived from the mouse monoclonal antibody (Mab) CRM01 and the remaining immunoglobulin-derived parts of the HAM are derived from a human immunoglobulin (or an analogue). The HAM was used for in vivo diagnosis and therapy of carcinomas of ovary, breast, uterus and lung.		
CC	CC Sequence 139 AA;		
CC	Query Match 75.0% Score 642; DB 7; Length 139;		
CC	Best Local Similarity 73.3%; Pred. No. 1.75e-40;		
CC	Matches 88; Conservative 14; Indels 2; Gaps 1;		
Db	20 qiqivqsgaevikkgasvksckasgstsyyihwrgapgglewgyidpfngtsty 79		
Qy	1 QVQLVQSGAEVKKGASVKSCKASGSTSYYIHWRGAPGGLEWMGRIDPSEGSDY 60		
Db	80 nekkfkgrytvstntaymellssldtaayccarggdifyandywggtlytvss 139		
Qy	61 VEKEFKKVTLTADTSSTAYMELSSLTDDTAVYYCAR-GKENVRFAYWGQTLTVYVSS 118		
RESULT	9		
ID	W29753 standard; Protein; 139 AA.		
AC	W29753;		(first entry)
DT	14-JAN-1998		
DE	CDR grafted humanised antibody heavy chain variable region 9H1.		
KW	Humanised antibody; CDR grafted antibody; Chimeric antibody; CTM01; complementary determining region; human milk fat globule; HMFG;		
KW	monoclonal antibody; Mab; mouse; cancer; breast cancer; ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy.		
KW	Chimeric Homo sapiens.		
KW	Chimeric Mus musculus.		
OS	Chimeric synthetic.		
OS	Key		
FT	Region 45..54		/note= "complementarity determining region 2 from CTM01"
FT	Region 118..128		/note= "CDR1 from CTM01"
FT	Region 116..126		/note= "complementarity determining region 3 from CTM01"
FT	Misc-difference 2		
FT	Misc-difference 37		
FT	Misc-difference 37		
FT	Location/Qualifiers		

FT Misc-difference 71 /note= "murine residue"
 FT Misc-difference 73 /note= "murine residue"
 FT Misc-difference 94 /note= "murine residue"
 FT Misc-difference 103 /note= "murine residue"
 FT Misc-difference 104 /note= "murine residue"
 FT Misc-difference 105 /note= "murine residue"
 FT Misc-difference 107 /note= "murine residue"
 FT EP-781B45-A2.
 PD 02-JUL-1997.
 PF 24-SEP-1992; 308680.
 PA (CILT) CELLTECH THERAPEUTICS LTD.
 PI Adair JR., Baker TS., Hamann PR., Hinman LM., Lyons AH;
 PI Menendez AT., Owens RJ;
 DR WPI; 97-334902/31.
 PT DNA encoding composite heavy and light chains of humanised antibody
 PT - specific for human milk fat globule, useful in cancer diagnosis or
 PT disclosure; Page 27; 53pp; English.
 PS This polypeptide sequence comprises gH1, a humanised antibody heavy
 CC chain variable region (VH) containing complementarity determining
 CC regions (CDRs) from the mouse anti-human milk fat globule (HMFG)
 CC monoclonal antibody CRM01 VH (see W29750) in a human EU framework
 CC modified to include some murine residues. It can be expressed in
 CC transformed host cells using a nucleotide sequence assembled from 8
 CC synthetic oligonucleotides (see T85858-65). A CDR-grafted VL chain
 CC (see W29754) has also been constructed. Anti-HMFG humanised VL chain
 CC antibodies can be conjugated with labels or drugs (especially
 CC methyltrithio antitumour agents) and used for the diagnosis or
 CC of human carcinomas, e.g. of the ovary, breast, uterus and lung.
 SQ Sequence 139 AA;

Query Match 75.0%; Score 642; DB 25; Length 139;
 Best Local Similarity 73.3%; Pred. No. 1.75e-40;
 Matches 14; Conservative 16; Indels 2; Gaps 1;

DB 20 qiqlvgsgaeikvkgpgssykvskicasqgtftdtyinwmgapgglewmgwidsgsgntky 79
 QY 1 QYQIVQSSAEVKPGASTRVSKIASGTYTEYMYWWQAPPQGLELMGRIDBEDGSIDY 60
 DB 80 nafkfgrytltvdtsntaymalslsredtafycarekttyyyandwygggtlvttvss 139
 QY 61 VKEFKKKVTLADTSSTAYMELSSLTSDTAVYYCARGK-F-NRYRAYWQGTLYVSS 118

RESULT 10
 ID W05825 standard; Protein; 120 AA.
 AC W31615; standard; Protein; 139 AA.
 DT 27-JAN-1997 (first entry)
 DE Humanised M291 antibody heavy chain variable region.
 KW B-cell lymphoma; myeloma; leukaemia; hybridoma;
 KW monoclonal antibody.
 OS Chimeric Homo sapiens;
 FH Key
 FT region 31..35
 FT /label= CDR1
 FT 50..66
 FT /label= CDR2
 FT 79..109
 FT /label= CDR3
 FT misc_difference 30
 FT /note= "human framework residue 30 is substd. by equivalent murine framework residue"
 FT misc_difference 44

FT FT /note= "human framework residue 44 is substd. by equivalent murine framework residue"
 FT misc_difference 67
 FT FT /note= "human framework residue 67 is substd. by equivalent murine framework residue"
 FT misc_difference 68
 FT FT /note= "human framework residue 68 is substd. by equivalent murine framework residue"
 FT misc_difference 70
 FT FT /note= "human framework residue 70 is substd. by equivalent murine framework residue"
 FT misc_difference 72
 FT FT /note= "human framework residue 72 is substd. by equivalent murine framework residue"
 FT misc_difference 74
 FT FT /note= "human framework residue 74 is substd. by equivalent murine framework residue"
 PN W09626964-A1.
 PD 06-SEP-1996.
 PF 29-FEB-1996; 002754.
 PR 01-MAR-1995; US-397411.
 PA (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
 PA (PRON-) PROTEIN DESIGN LABS INC.
 PI Gingrich R, Link BK, Tso JY, Weiner G;
 DR WPI; 96-11274/41.
 PT New bispecific antibody reactive with both T or NK cells and
 PT malignant B cells - also their humanised forms and hybridomas
 PT producing them, useful for treating or preventing leukaemia,
 PT lymphoma and myeloma.
 PS Claim 18, Fig 5b; 85pp; English.
 CC The variable region (W05825) of the humanised M291 heavy chain variable
 CC chain (W05826) consists of human HF2-1/17 heavy chain variable
 CC region framework and complementarity determining regions from the
 CC murine M291 antibody specific for CD3 antigen. It can be
 CC coexpressed with humanised M291 light chain (see also W05830) in
 CC mammalian host cells. Humanised antibody fragments can be
 CC incorporated into novel bispecific antibodies reactive with both
 CC effector cell antigens and malignant B-cells (see also W05822-23,
 CC W05828-29).
 SQ Sequence 120 AA;

Query Match 74.5%; Score 638; DB 20;
 Best Local Similarity 76.7%; Pred. No. 3.63e-40;
 Matches 92; Conservative 18; Indels 2; Gaps 2;

Db 1 qvqlvqsgaeikvkgpgssykvskicasqgtftdtyinwmgapgglewmgwidsgsgntky 60
 QY 1 QVQLVQSGAEVKPGASTRVSKIASGTYTEYMYWWQAPPQGLELMGRIDBEDGSIDY 60
 Db 61 nqkLkdkatltdksasataymelslsredtafycarekttyyyandwygggtlvttvss 120
 QY 61 VEKFKKVTLADTSSTAYMELSSLTSDTAVYYCARGK-F-NRYRAYWQGTLYVSS 118

RESULT 11
 ID W31615; standard; Protein; 139 AA.
 AC W31615;
 DT 22-MAY-1998 (first entry)
 DE Humanised heavy chain variable region of mouse M291 antibody.
 KW Heavy chain; variable region; low mitogenic response; human T-cell;
 KW immunosuppressant; diagnosis; immune system disease; antibody M291;
 KW humanised, mouse; murine.
 OS Mus sp.
 OS Synthetic.
 FH Key
 FT Region 50..54
 FT /note= "complementarity determining region 1"
 FT Region 69..85
 FT /note= "complementarity determining region 2"
 FT Region 118..128
 FT /note= "complementarity determining region 3"
 PD WO744362-A1.
 PN 27-NOV-1997.

PR 19-MAY-1997; US8576.
 PR 31-MAY-1996; US-656586.
 PR 20-MAY-1996; US-650410.
 PA (HUTCHINSON CANCER RES CENT FRED.
 PA (PROTEIN DESIGN LABS INC.
 PI Anasetti C, Cole MS, Tso JY;
 DR WPI; 98-018436/02.
 DR N-PSDB; V01095.
 PT Mutated immunoglobulin G 2 constant region that does not induce T cell proliferation - and anti-CD3 antibodies containing this region for use as immunosuppressants with reduced side effects
 PS Claim 11; Fig 1D; 63pp; English.
 CC The present sequence was used in the development of a novel mutated immunoglobulin G (IgG) 2 constant region (CR) having a non-natural segment of amino acids between 234 and 237 (EU numbering system), so that an antibody (Ab) containing the variable region of an anti-CD3 Ab linked to the CR induces a lower mitogenic response in human T-cells than does a similar Ab containing the natural IgG2 constant region.
 CC The Ab are useful as immunosuppressants, e.g. in autoimmune disease (including rheumatoid arthritis, multiple sclerosis, type I diabetes, systemic lupus erythematosus and inflammatory bowel disease), transplant rejection, graft versus host disease, inflammation allergy or sepsis, particularly acute episodes of autoimmune diseases. The Ab can also be used for diagnosis of immune system disease. And for determining T cell numbers in patients with acquired immune deficiency syndrome (AIDS).
 CC The Ab have fewer side effects than known anti-CD3 Ab, as they do not, in most patients, induce mitogenesis through specific binding to Fc gamma receptors, nor release of cytokines. Compared with F(ab')2 fragments, the Ab have a longer half-life.
 SQ Sequence 139 AA;

Query Match Best Local Similarity 76.7%; Score 638; DB 28; Length 139; Pred. No. 3 63e-40; Matches 92; Mismatches 18; Indels 2; Gaps 2;

Db 20 qvqlvqsgaevkkpgasvkvsckasqytfsytmhwrqapgglewmgynprsgthy 79
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASQYTFSYTMHWRQAPGGLEMLGRIDPEGSIDY 60
 Db 80 nqklkdkatltadksastaymelssrsedtavtycarsyydydfayrggtlvttss 139
 QY 61 VEKFKKVLTADTSSTAMELSSRSDDTAVYCARGF-NTR-FAVNGQGLTVYSS 118

RESULT 12 ID W05826 standard; Protein; 279 AA.
 AC W05826;
 DT 27-JAN-1997 (first entry)
 DE Humanised M291 antibody heavy chain.
 KW CD3 antigen; humanised antibody; bispecific antibody;
 KW B-cell lymphoma; myeloma; leukaemia; hybridoma;
 KW monoclonal antibody.
 OS Chimeric Homo sapiens;
 FH Key
 FT domain 1..120 /label= Variable_domain
 FT region 31..35 /label= CDR1
 FT region 50..66 /label= CDR2
 FT region 79..109 /label= CDR3
 FT misc_difference 30 /note= "human framework residue 30 is substd. by equivalent murine framework residue"
 FT misc_difference 44 /note= "human framework residue 44 is substd. by equivalent murine framework residue"
 FT misc_difference 67 /note= "human framework residue 67 is substd. by equivalent murine framework residue"

FT misc_difference 68 /note= "human framework residue 68 is substd. by equivalent murine framework residue"
 FT misc_difference 70 /note= "human framework residue 70 is substd. by equivalent murine framework residue"
 FT misc_difference 72 /note= "human framework residue 72 is substd. by equivalent murine framework residue"
 FT misc_difference 74 /note= "human framework residue 74 is substd. by equivalent murine framework residue"
 FT misc_difference 121..218 /label= CH1_domain
 FT domain 219..238 /label= Hinge_domain
 FT domain 239..279 /label= Fos_leucine_zipper

PN W0562964-A1.
 PD 06-SEP-1996.
 PF 29-FEB-1996; US2754.
 PR 01-MAR-1995; US-397411.
 PA (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
 CC (PROT-) PROTEIN DESIGN LABS INC. PI Gingrich R, Link BK, Tso JY, Weiner G; DR WPI; 96-41274/41.
 PT New bispecific antibody reactive with both T or NK cells and malignant B cells - also their humanised forms and hybridomas, producing them, useful for treating or preventing leukaemia, lymphoma and myeloma.
 PS Claim 28; Fig 5d; 85pp; English.
 CC The humanised M291 antibody heavy chain (W05826) includes a variable region (see also W05825) consisting of human HF2-1/17 heavy chain variable region framework and complement determining regions from the murine M291 antibody specific for CD3 antigen. It can be coexpressed with humanised M291 light chain (see also W05830) in mammalian host cells. Bispecific antibodies can be constructed that include a first binding fragment comprising humanised M291 heavy and light chain variable regions, and a second binding fragment comprising humanised 1D10 heavy and light chain variable regions (see also W05828-29). Such antibodies are reactive with both T or NK cells and malignant B cells, and have therapeutic application.

Query Match Best Local Similarity 74.5%; Score 638; DB 20; Length 279; Pred. No. 3 63e-40; Matches 92; Mismatches 18; Indels 2; Gaps 2;

Db 1 qvqlvqsgaevkkpgasvkvsckasqytfsytmhwrqapgglewmgynprsgthy 60
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASQYTFSYTMHWRQAPGGLEMLGRIDPEGSIDY 60
 Db 61 nqklkdkatltadksastaymelssrsedtavtycarsyydydfayrggtlvttss 120
 QY 61 VEKFKKVLTADTSSTAMELSSRSDDTAVYCARGF-NTR-FAVNGQGLTVYSS 118

RESULT 13 ID W26651 standard; Protein; 382 AA.
 AC W26651;
 DT 12-FEB-1998 (first entry)
 DE Chimeric receptor hCTMOL/h/zeta.
 KW IgG1; T cell receptor zeta chain; cell proliferation; cytokine; Cell activation; chimeric receptor; DNA delivery; CTMOL; scFv;
 KW inflammation; effector; cell differentiation; antibody secretion; Phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW phagocytosis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes; graft versus host disease; human; therapy.
 OS Chimeric - Homo sapiens.

DR WPI: 97-351052/32.
 DR N-PSDBL T90511
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS Disclosure; Fig 6: 90pp; English.
 CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTM01 linked to an
 CC extracellular spacer from part of human CD8 hinge, linked to the
 CC intracellular and intracellular components of human CD28. It can
 CC be expressed in host cells using a chimeric receptor gene (see
 CC T90511) constructed from DNA cassettes of each component. In a
 CC claimed cell activation process an effector cell is transformed with
 CC DNA encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/idiopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 SQ sequence 403 AA;

Query Match	Score 73.88;	Length 403;
Best Local Similarity 72.5%	Pre. No. 1.08e-39;	
Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1		
Db 160 qiqivqsgaeavkkpgssykvskasqytfttdyyinwmrqapggglewigwividpgqntky 219		
Qy 1 QqvlvQSGAEVKKPGSSYKVSKASQYTFTTDYYINWMRQAPGGGLEWIGWIVIDPGQNTKY 60		
Db 220 nefkgrstltvatsttaytmelssrlssetafccarekttyyyamdryqeggltvvss 279		
Qy 61 VEFKKVYLTAQTSSSTAYMELSSRLSSETAFCCAREKTYYYAMDYQEGGLTVVSS 118		

RESULT 15
 ID W26646 standard: Protein; 473 AA.
 AC W26646;
 DT 12-FEB-1998 (first entry)
 DE Chimeric receptor CTM01/CD8/zeta.
 KW Cell activation; chimeric receptor; DNA delivery; CTM01; scFv; CD8;
 KW T cell receptor zeta chain; cell proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.
 OS Chimeric - Homo sapiens.
 PN W09723613-A2.
 PD 03-JUL-1997
 PF 23-DEC-1996; G03209.
 PR 21-DEC-1995; GB-026131.
 PA (CELLTECH THERAPEUTICS LTD.
 DR Bebbington CR, Finney HM, Lawson ADG, Well ANC;
 DR WPI: 97-351052/32.
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS Disclosure; Fig 4: 90pp; English.
 CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTM01 linked to an

extracellular spacer in the form of part of human CD8 hinge, linked to the extracellular, transmembrane and intracellular components of the human T cell receptor zeta chain. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (see T90509) constructed from DNA cassettes of each component. In a claimed cell activation process an effector cell is transformed with DNA encoding a chimeric receptor containing 2 or more different cytoplasmic signalling components. Also claimed is use of DNA encoding a recombinant chimeric receptor in a DNA delivery system. The DNA delivery systems can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytokines with e.g. pro- or anti-inflammatory responses, stimulation of cytolytic activity, differentiation or other effector functions, antibody secretion, phagocytosis, tumour infiltration and/or increased adhesion. They can be used in the treatment of e.g. infectious disease, inflammatory disease, cancer, allergic/atopic disease, congenital disease, dermatologic disease, neurologic disease, transplants and metabolic/idiopathic disease (claimed). In particular, they can be used in the treatment of rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, asthma, eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple sclerosis, organ or tissue transplant rejection, graft-versus-host disease or diabetes (claimed).

Sequence 473 AA;

Query Match 73 8%; Score 632; DB 25; Length 473;

Best Local Similarity 72.5%; Pred. No. 1.08e-39;
Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;

Db 160 qiglvsggevkpgssvkvsckasgystfdyyinwmgapgglewigwidpsgnhty 219
Qy 1 QWQLVQSGAEVKKGASVRSCKASGYTTEYYWWROAPGQHIELMGRIDPEDGSDY 60

Db 220 nekitkgralitvdtsntaymeisslrsedtafcarekttyyamdrwggtlytrss 279

Qy 61 VEKFKKVTLADFSSTAYMELSSLTDDTAVYCARGK-FNYRFAYWGQLVTVSS 118

Search completed: Thu Jan 14 17:15:38 1999
Job time : 31 secs.